

BGS 101, Absent lower laterals 1, *als1*

Stock number: BGS 101
Locus name: Absent lower laterals 1
Locus symbol: *als1*

Previous nomenclature and gene symbolization:

Absent lower laterals = *als* (2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 3HL (2, 3, 5, 6); about 31.2 cM distal from the *uzu1* (*uzu* 1) locus (2), about 39.7 cM proximal from the *cur2* (*curly* 2) locus (3); near AFLP marker E4234-11 in subgroup 28 of the Proctor/Nudinka map (4).

Description:

Lateral spikelets at the base of the spike fail to develop or are partially developed. Tillers are large, coarse, and stiff, and only 1 or 2 tillers are produced in the six-rowed stock. The plants resemble those of the (*cul2*) unculm 2 mutant (2). Plants of the Bowman backcross-derived line commonly produce 3 to 5 tillers with short spikes; and seed yields are very low (1).

Origin of mutant:

A gamma-ray induced mutant in Montcalm (CIho 7149) (2).

Mutational events:

als1.a (Alb Acc 281, GSHO 1065) in Montcalm (CIho 7149) (2).

Mutant used for description and seed stocks:

als1.a in Montcalm (GSHO 1065); *als1.a* in Bowman (PI 483237)*7 (GSHO 1990, BW012, NGB 20420).

References:

1. Babb, S., and G.J. Muehlbauer. 2003. Genetic and morphological characterization of the barley unculm 2 (*cul2*) mutant. *Theor. Appl. Genet.* 106:846-857.
2. Kasha, K.J., and G.W.R. Walker. 1960. Several recent barley mutants and their linkages. *Can. J. Genet. Cytol.* 2:397-415.
3. Konishi, T., J. Hayashi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley. VII. Location of six new mutant genes on chromosome 3. *Ber. Ohara Inst. landw. Biol., Okayama Univ.* 18:251-264.
4. Pozzi, C., D. di Pietro, G. Halas, C. Roig, and F. Salamini. 2003. Integration of a barley (*Hordeum vulgare*) molecular linkage map with the position of genetic loci hosting 29 developmental mutants. *Heredity* 90:390-396.
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6. Singh, R.J., and T. Tsuchiya. 1974. Further information on telotrisomic analysis in barley. *Barley Genet. Newsl.* 4:66-69.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:123.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:135.

J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:219.

BGS 102, Uzu 1, *uzu1*

Stock number: BGS 102
Locus name: Uzu 1 (semi-brachytic)
Locus symbol: *uzu1*

Previous nomenclature and gene symbolization:

Normal vs *uzu* = *h* (16).
Uzu = *u* (7).
Uzu (semi-brachytic) = *uz* (15).
Uzu 2 = *uz2* (6, 17, 19).
Uzu 3 = *uz3* (6, 17, 19).
Hordeum vulgare BR-insensitive 1 = *HvBRI1* (1).

Inheritance:

Monofactorial recessive (7, 11, 13, 15).
Located in chromosome 3HL (9, 10, 15); about 17.6 cM proximal from the *alm1* (albino lemma 1) locus (14); in bin 3H 06 near cDNA marker C1271 (1); about 10.1 cM from AFLP marker E3733-6 in subgroup 27 of the Proctor/Nudinka map (8); *uzu1.a* is associated with SNP markers 1_0373 to 1_1314 (positions 92.55 to 107.40 cM) in 3H bins 06 to 07 of the Bowman backcross-derived line BW885 (2); *uzu1.a* with *sld1.a* is associated with SNP markers 1_0653 to 2_0115 (positions 92.55 to 126.83 cM) in 3H bins 06 to 08 of the Bowman backcross-derived line BW860 (2); *uzu1.a* with *wst1.c* is associated with SNP markers 1_1258 to 2_0155 (positions 79.88 to 229.92 cM) in 3H bins 05 to 15 of the Bowman backcross-derived line BW912 (2); BW860, BW885, and BW912 have a common SNP marker pattern from 1_1191 to 2_0931 (positions 98.41 to 104.39 cM) in 3H bin 06 (2), in 3H bin 06.

Description:

The *uzu1.a* gene has pleiotropic effects on the elongation of the coleoptile, leaf, culm, rachis internode, awn, glume, and kernel (12, 13, 15). These organs are often reduced in length and increased in width. Changes in organ length are temperature sensitive, but heading date and maturity are unaltered. The coleoptile of *uzu* plants shows a prominent projection or hook near the apex. Sometimes the coleoptile of the mutant shows a V-shaped notch on the side opposite from the projection. Thus, the apex of the coleoptile has two notches, one on each side (13, 17, 18). The temperature sensitive reduction in culm length of *uzu1.a* plants ranged from less than 15% in cool environments to over 75% in warm ones. The Bowman backcross-derived line for *uzu1.a*, BW885, produced plants that were 20 to 40% shorter than Bowman, awns were about 1/3 of normal length, rachis internodes were shorter, 3.0 vs. 4.7 mm, and leaf blades were shorter and wider. Kernels of BW885 were shorter, 7.9 vs. 9.5 mm, and lighter, averaged 4.7 vs. 5.7 mg. Spikes of BW885 often had 2 more kernels than those of Bowman. Grain yields of BW885 ranged from 1/3 to 3/4 those of Bowman (3). Chono et al. (1) reported that the *uzu1.a* or *HvBRI1* gene is caused by a mutation that changed a highly conserved residue of the kinase domain of *BRI1* (*Arabidopsis* BR-insensitive 1) (brassinosteroids) receptor protein from His-857 to Arg-857. A second mutant in the *HvBRI1* gene was identified by Gruszka et al. (5).

Origin of mutant:

Natural occurrence in many cultivars of Japanese origin (12, 13).

Mutational events:

uzu1.a (OUJ371, PI 182624, GSHO 1300) in many Japanese cultivars (13, 17, 19);
uzu1.b (092AR) in Aramir (PI 467781) (4, 5).

Mutant used for description and seed stocks:

uzu1.a (OUJ371, PI 182624, GSHO 1300) in Baitori 11 (OUJ 043); *uzu1.a* from R.I. Wolfe's Multiple Marker Stock for chromosome 3 in Bowman (PI 483237)*7 (GSHO 1963, BW885, NGB 20787); *uzu1.a* with *wst1.c* (OUL074, GSHO 569) from Akashinriki (PI 467400, OUJ659) in Bowman*8 (GSHO 1967, BW912, NGB 22348); *uzu1.a* with *sld1.a* (OUM148, GSHO 2489) from Akashinriki in Bowman*8 (GSHO 1971, BW860, NGB 22397).

References:

1. Chono, M., I. Honda, H. Zeniya, K. Yoneyama, D. Saisho, K. Takeda, S. Takatsuto, T. Hoshino and Y. Watanabe. 2003. A semidwarf phenotype of barley *uzu* results from a nucleotide substitution in the gene encoding a putative brassinosteroid receptor. *Plant Physiol.* 133:1209-1219.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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5. Gruszka, D., I. Szarejko, and M. Maluszynski. 2011. New allele of *HvBR1* gene encoding brassinosteroid receptor in barley. *J. Appl. Genet.* 52:257-268.
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Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:124.

Revised:

T. Tsuchiya. 1984. Barley Genet. Newsl. 14:92.
J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:136-137.
J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:220-221.
J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:94-96.

BGS 104, Yellow streak 1, *yst1*

Stock number: BGS 104
Locus name: Yellow streak 1
Locus symbol: *yst1*

Previous nomenclature and gene symbolization:

Yellow stripe = *ys* (4).

Yellow streak = *yst* (5).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 3HS (3, 4, 6); about 2.9 cM proximal from the *zeb1* (zebra stripe 1) locus (3); 7.6 cM proximal from the *uzu1* (*uzu* 1) locus (3); *yst1.a* is associated with SNP markers 2_0410 to 2_1511 (positions 64.85 to 92.56 cM) in 3H bins 05 to 06 of the Bowman backcross-derived line BW924 (1).

Description:

Longitudinal yellow stripes appear on seedling leaves and persist until the preripening stage. In some crosses and under certain environmental conditions, the most heavily striped F₂ plants fail to reach maturity. There is no evidence for a cytoplasmic association in the inheritance patterns (4). Expression of the *yst1.a* allele in the Bowman backcross-derived line, BW924, is reduced to very narrow streaks that occur infrequently (2). Other deviations from the Bowman phenotype were not observed (2).

Origin of mutant:

A DDT induced mutant in Gateway (CIho 10072) (4).

Mutational events:

yst1.a (GSHO 1140) in Gateway (CIho 10072) (4).

Mutant used for description and seed stocks:

yst1.a (GSHO 1140) in Gateway; *yst1.a* in Bowman (PI 483237)*7 (GSHO 1959, BW924, NGB 22353).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:126.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:138.

J.D. Franckowiak. 2012. *Barley Genet. Newsl.* 42:178.

BGS 105, Xantha seedling 3, *xnt3*

Stock number: BGS 105
Locus name: Xantha seedling 3
Locus symbol: *xnt3*

Previous nomenclature and gene symbolization:

Xantha seedling c = x_c (1).

Viridis seedling-I = *vir-I* (3).

Inheritance:

Monofactorial recessive (1).

Located in chromosome 3HS (5, 6); about 9.4 cM proximal from the *abo9* (albino seedling 9) locus (2); about 14.4 cM distal from the *uzu1* (*uzu* 1) locus (5, 6); about 3.7 cM proximal from the *alm1* (albino lemma 1) locus (5).

Description:

Seedlings have a yellow (picric yellow) to yellow-green color depending upon temperatures, but they can be grown to maturity under certain environmental conditions (1). The *xnt3.c* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in Colseess (CIho 2792) (1).

Mutational events:

xnt3.c (Colseess IV, GSHO 66) in Colseess (CIho 2792) (1); *vir-I.27* (NGB 14701) in Maja (PI 184884) (4, 7).

Mutant used for description and seed stocks:

xnt3.c (GSHO 66) in Colseess.

References:

1. Robertson, D.W. 1929. Linkage studies in barley. *Genetics* 14:1-36.
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Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:127.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:139.

BGS 106, Albino seedling 6, *abo6*

Stock number: BGS 106
Locus name: Albino seedling 6
Locus symbol: *abo6*

Previous nomenclature and gene symbolization:

White seedling $c = a_c$ (2).

Albino seedling $c = a_c$ (3).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 3HS (4); about 10.7 cM distal from the *uzu1* (*uzu 1*) locus (4);

about 2.4 cM from the *msg5* (male sterile genetic 5) locus (1).

Description:

Seedlings are white in color, devoid of normal pigments, and die about 10 days after emergence (2). Plants with this phenotype are classified as albino mutants (3). The *abo6.f* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in Colseess (CIho 2792) (2).

Mutational events:

abo6.f (Colseess III, GSHO 63) in Colseess (CIho 2792) (2); Colseess I and Colseess II in Colseess (2).

Mutant used for description and seed stocks:

abo6.f (GSHO 30) in Colseess.

References:

1. Rahman, M.M., and R.F. Eslick. 1975. Linkage of male sterile genes with seedling lethal genes. *Barley Genet. Newsl.* 5:42-44.
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Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:128.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:140.

BGS 107, White steak 1, *wst1*

Stock number: BGS 107
Locus name: White streak 1
Locus symbol: *wst1*

Previous nomenclature and gene symbolization:

White stripe = *wst* (5).
Stripe = *st* (3, 6).
White streak 3 = *wst3* (8, 9, 10, 12, 13).

Inheritance:

Monofactorial recessive (3, 6, 10).
Located in chromosome 3HL (5, 7, 9, 14); very close to the *uzu1* (*uzu* 1) locus (3, 8, 9, 13); *wst1.a* is associated with SNP markers 2_0968 to 1_0584 (positions 46.19 to 178.12 cM) in 3H bins 04 to 11 of the Bowman backcross-derived line BW910 (1); *wst1.c* with *uzu1.a* is associated with SNP markers 1_1258 to 2_0155 (positions 79.88 to 229.92 cM) in 3H bins 05 to 15 of the Bowman backcross-derived line BW912 (1).

Description:

Very narrow white stripes are present in the leaves from the seedling stage until near maturity. Plants have nearly normal vigor (4). The size of the white sectors is variable from mutant to mutant, plant to plant, and leaf to leaf. All affected plants may produce albino seedlings among their selfed progeny with reported frequencies between 1.0 and 25.6% (9, 11). Albino seedlings have not been observed when *wst1* plants were used as the male parent in crosses (9, 11). Caldecott's streak has wider and larger white sectors and produces a higher frequency of albino seedlings (11). Compared to Bowman, plants of the Bowman backcross-derived line for *wst1.a*, BW910, headed 3 to 4 days later and were slightly shorter, but the awns were slightly longer. The kernels of BW910 were slightly narrower, 3.7 vs. 3.9, and lighter than the Bowman kernels in many trials. The test weights and grain yields for BW910 were slightly reduced (2).

Origin of mutant:

A spontaneous mutant in an unknown cultivar (3, 8, 11); a radiation induced mutant (8, 9, 10, 11, 12).

Mutational events:

wst1.a (USDA 163, Clho 11767, GSHO 159) in an unknown cultivar (4); *wst1.c* (OUL074, GSHO 569) in Akashinriki (PI 467400, OUJ659) (9, 10, 11, 12); *wst1.e* in Himalaya (GSHO 278, Caldecott's streak) (10, 14); *wst1.f* (Grandpa fine stripe) in an unknown cultivar (Clho 6856, GSHO 854), *wst1.g* in Clho 6758 (GSHO 314) (10); *wst1.h* in Clho 11766 (GSHO 797) (4, 10); *wst1.i* in Moravian (PI 537135) (10).

Mutant used for description and seed stocks:

wst1.a (GSHO 159, Clho 11767) in an unknown cultivar; *wst1.a* in Bowman (PI 483237)*6 (GSHO 1966); *wst1.a* in Bowman*7 (BW910, NGB 22341); *wst1.c* with *uzu1.a* (OUL074, GSHO 569) from Akashinriki (PI 467400, OUJ659) in Bowman*8 (GSHO 1967, BW912, NGB 22343).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Kasha, K.J., and G.W.R. Walker. 1960. Several recent barley mutants and their linkages. *Can. J. Genet. Cytol.* 2:397-415.
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species). Crop Sci. 7:41-42.

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Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:129.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl. 10:110.

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:141-142.

J.D. Franckowiak. 2011. Barley Genet. Newsl. 41:97-98.

BGS 108, Albino lemma 1, *alm1*

Stock number: BGS 108
Locus name: Albino lemma 1
Locus symbol: *alm1*

Previous nomenclature and gene symbolization:

Albino lemma = *al* (9).

Eburatum = *ebu-a* (3).

Inheritance:

Monofactorial recessive (9).

Located in chromosome 3HS (9); about 16.5 cM distal from the *uzu1* (*uzu 1*) locus (2, 5, 6, 7, 8, 9); about 4.8 cM proximal from RFLP marker MWG844B in 3H bin 04 (1).

Description:

The lemma and palea are white in color and mostly devoid of chlorophyll, but they terminate into green tips with green awns. The basal part of lower leaf sheaths and stem nodes are devoid of chlorophyll. Ligules and joints between the leaf sheath and blade are white in color (9, 10). Plant vigor is reduced slightly and maturity is delayed in the Bowman backcross-derived line.

Origin of mutant:

Spontaneous occurrence in an unknown cultivar (Russia 82) (OUU086, NSL 43389) (9).

Mutational events:

alm1.a (GSHO 270) in Russia 82 (OUU086, NSL 43389) (9); *alm1.b* in Liberty (Clho 9549) (2); *alm1.c* (Mut 966/61) in Proctor (PI 280420) (4); *ebu-a.1* (NGB 115236), *-a.2* (NGB 115237), *-a.3* (NGB 115238) in Foma (Clho 11333) (3, 10); *ebu-a.4* (NGB 115239), *-a.5* (NGB 115240) in Foma (6).

Mutant used for description and seed stocks:

alm1.a (GSHO 270) in Russia 82; *alm1.a* in Bowman (PI 483237)*8 (GSHO 1953, BW011, NGB 20419).

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mutants. Barley Genet. Newsl. 3:67-68.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:130.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl. 10:111.

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:143.

J.D. Franckowiak and U. Lundqvist. 2007. Barley Genet. Newsl. 37:222-223.

BGS 109, Yellow streak 2, *yst2*

Stock number: BGS 109
Locus name: Yellow streak 2
Locus symbol: *yst2*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 3HS (1, 2, 3); about 0.9 cM distal from the *alm1* (albino lemma 1) locus (2).

Description:

When grown at low temperatures, seedlings develop numerous wide yellow streaks in the seedling leaves. Exposure to 3EC for two weeks after sowing induces distinct streaks in the first and second leaves. As temperatures rise, newly developed leaves have only very fine yellow streaks (2). These streaks persist until the plant nears maturity. As plants develop, they have a yellow-green color, show delayed maturation, and have low seed yields.

Origin of mutant:

A spontaneous mutant in the F₅ generation of the cross Kuromugi 148 (OUJ646)/Mensury C (OUJ732) (2).

Mutational events:

yst2.b (GSHO 570) in Kuromugi 148/Mensury C (OUJ073) (2).

Mutant used for description and seed stocks:

yst2.b (GSHO 570) in Kuromugi 148/Mensury C (OUJ073); *yst2.b* in Bowman (PI 483237)*7 (GSHO 1952, BW925, NGB 22354).

References:

1. Singh, R.J., and T. Tsuchiya. 1974. Further information on telotrisomic analysis in barley. *Barley Genet. Newsl.* 4:66-69.
2. Takahashi, R., and I. Moriya. 1969. Inheritance and linkage studies in barley. IV. Linkages of four variegated mutants. *Ber. Ohara Inst. landw. Biol., Okayama Univ.* 15:35-46.
3. Tsuchiya, T., and R.J. Singh. 1973. Further information on telotrisomic analysis in barley. *Barley Genet. Newsl.* 3:75-78.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:131.

Revised:

J.D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:144.

BGS 111, Dense spike 10, *dsp10*

Stock number: BGS 111
Locus name: Dense spike 10
Locus symbol: *dsp10*

Previous nomenclature and gene symbolization:

Dense spike $c = l_c$ (6, 8).

Inheritance:

Monofactorial recessive (2, 8).

Located in chromosome 3HL (2, 5, 8); about 1.3 cM distal from the *xnt3* (xantha seedling 3) locus (7, 8.); *dsp10.c* is associated with SNP markers 2_0002 to 1_0628 (positions 82.03 to 135.80 cM) in 3H bins 05 to 07 of the Bowman backcross-derived line BW278; *dsp10.ai* (previously *pyr.ai*) is associated with SNP markers 2_1109 to 2-1305 (positions 78.82 to 103.33 cM) in 3H bins 05 to 06 of the Bowman backcross-derived line BW655; *dsp10.aj* (previously *dsp.aj*) is associated with SNP markers 2_0794 to 1_0747 (positions 39.80 to 144.30 cM) in 3H bins 04 to 09 of the Bowman backcross-derived line BW258 (1); the region of 3H with common SNP markers retained all three stocks is from 2_002 to 1_0224 (positions 82.03 to 85.26) (1, 3), in 3H bin 05 near the centromere. A small common set of SNP markers 2_002 to 1_0925 (positions 82.03 to 84.19 cM) are preserved in dense spike variants from Steptoe: *dsp10.ba* (BW273), *dsp10.bb* (BW274), and *dsp10.bc* (BW275) (1, 3).

Description:

Although rachis internode length or spike density is not a highly stable character, plants with relatively dense spikes can be selected from crosses to Club Mariout. Rachis internode length values of 2.8 to 3.4 mm, 2.9 to 3.6 mm, and 2.6 to 2.8 mm were recorded for Club Mariout in one experiment (8). Plants in Bowman backcross-derived lines for *dsp10* locus (BW258, BW278, and BW655) had average rachis internode lengths of 3.3 mm compared to 4.6 mm for Bowman. The plants were 5 to 15% shorter than Bowman plants and spikes averaged 2 to 3 more kernels. Kernel weights and grain yields of the Bowman lines with *dsp10* were similar to values for Bowman (3).

Origin of mutant:

Natural occurrence in Club Mariout (CIho 261, PI 9877) (2, 8) and other cultivars (9).

Mutational events:

dsp10.c in Club Mariout (CIho 261, GSHO 71) (2, 8).

Mutant used for description and seed stocks:

dsp10.c in Club Mariout (GSHO 71, CIho 261, PI 9871); *dsp10.c* in Bowman (PI 483237)*3 (GSHO 1956), in Bowman*6 (BW278, NGB 20562); *dsp10.ai* from a 6-rowed line mutated in Sweden (18:08:04, GSHO 2433) (4) in Bowman*6 (GSHO 2241), in Bowman*7 (BW655, NGB 22220); *dsp10.aj* from a 6-rowed line mutated in Sweden (18:08:04, GSHO 1720) (4) in Bowman*5 (GSHO 2242), in Bowman*6 (BW258, NGB 22083); *dsp10.ba* from UT1713 (GSH1730) in Bowman*6 (GSHO2251), in Bowman*7 (BW273, NGB 22098); *dsp10.bb* from Steptoe mutant (Az34, GSHO2415) in Bowman*3 (BW274, NGB 22099); *dsp10.bc* from Steptoe mutant (FN4) in Bowman*4 (BW275, NGB 22100).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development1. *Plant Physiol.* 155:617-627.
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8. Webster, O.J. 1950. Genetic and morphologic studies of rachis internode length in barley. Ph.D. Thesis. Univ. of Minnesota, St. Paul.
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Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:133.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:145.

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:99-100.

BGS 112, Albino seedling 9, *abo9*

Stock number: BGS 112
Locus name: Albino seedling 9
Locus symbol: *abo9*

Previous nomenclature and gene symbolization:

White seedling n = a_n (2).
Albino seedling n = a_n (3).

Inheritance:

Monofactorial recessive (2).
Located in chromosome 3HS (1, 2); about 9.4 cM distal from the *xnt3* (xantha seedling 3) locus (2); about 15.5 cM proximal from the *xnt6* (xantha seedling 6) locus (2); about 9.9 cM distal from the *yst1* (yellow streak 1) locus (1).

Description:

Seedlings are white in color and devoid of normal pigments (2). Plants with this phenotype are classified as albino mutants (3). The *abo9.i* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in *Hordeum distichum* var *nigrinudum* (2).

Mutational events:

abo9.i (Nigrinudum I, GSHO 348) in Nigrinudum (NSL 3286, GSHO 988) (2).

Mutant used for description and seed stocks:

abo9.i (GSHO 348) in Nigrinudum.

References:

1. Kasha, K., and C.R. Burnham. 1965. The location of interchange breakpoints in barley. I. Linkage studies and map orientation. Can. J. Genet. Cytol. 7:62-77.
2. Robertson, D.W. 1937. Maternal inheritance in barley. Genetics 22:104-113.
3. Robertson, D.W., G.A. Wiebe, and F.R. Immer. 1941. A summary of linkage studies in barley. J. Am. Soc. Agron. 33:47-64.

Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:134.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:146.

BGS 113, Xantha seedling 6, *xnt6*

Stock number: BGS 113
Locus name Xantha seedling 6
Locus symbol: *xnt6*

Previous nomenclature and gene symbolization:

Xantha seedling s = x_s (2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 3HS (2); over 15.5 cM distal from the *abo9* (albino seedling 9) locus (2); over 15.3 cM distal from the *msg5* (male sterile genetic 5) locus (1); over 22.0 cM distal from the *wst1* (white streak 1) locus (3).

Description:

Seedlings have a bright yellow (citron green) to yellow-green color and do not survive beyond the seedling stage (2). The *xnt6.f* gene must be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in Smyrna (PI 7969) (2).

Mutational events:

xnt6.f (x_s) (Smyrna I, GSHO 117) in Smyrna (PI 7969) (2).

Mutant used for description and seed stocks:

xnt6.f (GSHO 117) in Smyrna.

References:

1. Rahman, M.M., and R.F. Eslick. 1975. Linkage of male sterile genes with seedling lethal genes. Barley Genet. Newsl. 5:42-44.
2. Robertson, D.W. 1937. Inheritance in barley. II. Genetics 22:443-451.
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Prepared:

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:135.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl. 10:112.

J.D. Franckowiak and A. Hang. 1997. Barley Genet. Newsl. 26:147.

BGS 114, Curly 2, *cur2*

Stock number: BGS 114
Locus name: Curly 2
Locus symbol: *cur2*

Previous nomenclature and gene symbolization:

Deformed plant, Bikini (2, 4).
Curly 2 = *cu2* (6).

Inheritance:

Monofactorial recessive (6, 7).
Located in chromosome 3HL (5, 6, 10); over 36.8 cM distal from the *als1* (absent lower laterals 1) locus (3, 6, 7); about 7.7 cM proximal from the *fch2* (chlorina seedling 2) locus (11).

Description:

The awn, lemma, and palea are extremely curly, the rachis is twisted slightly in most spikes, and the stem internodes are strongly curved. Leaves are short and severely twisted (3, 6). Roots are extremely curled compared to the straight roots of normal sister plants (9).

Origin of mutant:

A spontaneous mutant in Choshiro (OUJ451, CIho 190266) (3, 7).

Mutational events:

cur2.b (Choshiro-hen , OUL006, GSHO 274) in Choshiro (OUJ451, CIho 190266) (3, 6); *cur2.c* (dwarf 2) in an unknown cultivar (8); *cur2.d* (deformed plant, Bikini) in Bonus (PI 189763) (2, 4, 8); *cur2.g* (GSHO 1706) in Carina (PI 371632) (1).

Mutant used for description and seed stocks:

cur2.b (GSHO 274) in Choshiro; *cur2.b* in Bowman (PI 483237)*5 (GSHO 1991); *cur2.b* in Bowman *6 (BW220, NGB 22047); *cur2.g* in Bowman*5 (GSHO 1992); *cur2.g* in Bowman*5 (BW221, NGB 22048).

References:

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2. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
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Prepared:

T. Tsuchiya and T.E. Haus. 1971. *Barley Genet. Newsl.* 1:136.

Revised:

J.D. Franckowiak, T. Konishi, and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:148.

BGS 115, Non-brittle rachis 1, *btr1*

Stock number: BGS 115
Locus name: Non-brittle rachis 1
Locus symbol: *btr1*

Previous nomenclature and gene symbolization:

Non-brittle rachis = *r* (7).
Non-brittle rachis = *b* (2).
Non-brittle rachis 1 = *bt1* (1).

Inheritance:

Monofactorial recessive in crosses to *Hordeum vulgare* subsp. *spontaneum* (2, 3, 7).
Located in chromosome 3HS (5, 6); very close or semi-allelic to the *btr2* (non-brittle rachis 2) locus (5, 6); the *Btr1Btr2* complex is about 15.4 cM distal from the *alm1* (albino lemma 1) locus (6).

Description:

Joints at the rachis nodes are tough or non-brittle, which prevents segmentation or disarticulation of the rachis prior to maturity. Plants homozygous for the *btr1.a* allele do not shatter prior to harvest in contrast to wild barley (*Hordeum vulgare* subsp. *spontaneum*). All cultivars with the *btr1.a* allele have a dominant allele at the *Btr2* locus. When crossed to cultivars with the *btr2.b* allele at the *Btr2* locus (genotype *Btr1Btr1btr2btr2*), F₁ plants have a brittle rachis. The segregation ratio in the F₂ generation is 1 brittle : 1 tough rachis (5). The majority of the cultivars distributed in Occidental region of the Old World have the *btr1.a* allele (4, 6).

Origin of mutant:

Probably a spontaneous mutant in *Hordeum vulgare* subsp. *spontaneum*.

Mutational events:

btr1.a in an unknown race of *Hordeum vulgare* subsp. *spontaneum* (3, 6); the line A222 (CIho 11555) is recommended as the source line for the *btr1.a* gene.

Mutant used for description and seed stocks:

btr1.a in A 222 (GSHO 1233); *Btr1Btr2* from R.I. Wolfe's Multiple Dominant Marker Stock in Bowman (PI 483237)*10 (GSHO 1937, BW102, NGB 20508).

References:

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7. Ubisch, G. von. 1915. Analyse eines Falles von Bastardatavismus und Faktorenkoppelung bei Gerste. Z. Indukt. Abstammungs. Vererbungs. 14:226-237.

Prepared:

R. Takahashi. 1972. Barley Genet. Newsl. 2:181.

Revised:

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:149.

BGS 116, Non-brittle rachis 2, *btr2*

Stock number: BGS 116
Locus name: Non-brittle rachis 2
Locus symbol: *btr2*

Previous nomenclature and gene symbolization:

Non-brittle rachis = *r* (7).
Non-brittle rachis = *b* (2).
Non-brittle rachis 2 = *bt2* (1).

Inheritance:

Monofactorial recessive in crosses to *Hordeum vulgare* subsp. *spontaneum* (2, 3, 7).
Located in chromosome 3HS (5, 6); very close or semi-allelic to the *btr1* (non-brittle rachis 1) locus (5, 6); the *Btr1Btr2* complex is about 15.4 cM distal from the *alm1* (albino lemma 1) locus (6).

Description:

Joints at the rachis nodes are tough or non-brittle, which prevents segmentation or disarticulation of the rachis prior to maturity. Plants homozygous for the *btr2.b* allele do not shatter prior to harvest in contrast to wild barley (*Hordeum vulgare* subsp. *spontaneum*). All cultivars with the *btr2.b* allele have a dominant allele at the *Btr1* locus. When crossed to cultivars with the *btr1.a* allele at the *Btr1* locus (genotype *btr1btr1Btr2Btr2*), F₁ plants have a brittle rachis. The segregation ratio in the F₂ generation is 1 brittle : 1 tough rachis (5). The majority of the cultivars (mostly six-rowed) distributed in Oriental region of the Old World have the *btr2.b* allele (4, 6).

Origin of mutant:

Probably a spontaneous mutant in *Hordeum vulgare* subsp. *spontaneum*.

Mutational events:

btr2.b in an unknown race of *Hordeum vulgare* subsp. *spontaneum* (3, 6).

Mutant used for description and seed stocks:

btr2.b in Sakigoke (OUJ349, GSHO 842); *btr2.b* in Bowman (PI 483237); *Btr1Btr2* from R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1565) in Bowman*10 (GSHO 1937, BW102, NGB 20508).

References:

1. Johnson, I.J., and E. Åberg. 1943. Inheritance of brittle rachis in barley. J. Am. Soc. Agron. 35:100-106.
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3. Takahashi, R. 1955. The origin and evolution of cultivated barley. p. 227-266. In M. Demerec (ed.) Advances in Genetics, Vol. 7. Academic Press, New York.
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6. Takahashi, R., and J. Hayashi. 1964. Linkage study of two complementary genes for brittle rachis in barley. Ber. Ohara Inst. landw. Biol., Okayama Univ. 12:99-105.
7. Ubisch, G. von. 1915. Analyse eines Falles von Bastardatavismus und Faktorenkoppelung bei Gerste. Z. Indukt. Abstammungs. Vererbungs. 14:226-237.

Prepared:

R. Takahashi. 1972. Barley Genet. Newsl. 2:182.

Revised:

J.D. Franckowiak and T. Konishi. 1996. Barley Genet. Newsl. 26:150.

BGS 117, Chlorina seedling 2, *fch2*

Stock number: BGS 117
Locus name: Chlorina seedling 2
Locus symbol: *fch2*

Previous nomenclature and gene symbolization:

Chlorina seedling 2 = *f2* (9).
Light green 5 = *lg5* (8).
Chlorina seedling *f2* = *clo-f2* (5).

Inheritance:

Monofactorial recessive (1, 2, 9).
Located in chromosome 3HL (7, 9, 10, 11); about 7.7 cM distal from the *cur2* (curly 2) locus (12).

Description:

Seedlings have a pale yellow-green color, which persists until near maturity under greenhouse or field conditions. Development of homozygotes is delayed, but the stunted plants survive to produce seed (1). A complete absence or greatly reduced levels of chlorophyll *b* were found in mutant plants (1, 2, 5). The respiratory and photosynthetic rates of detached leaves and intact plants are not significantly different from those of normal plants. However, the growth rate of mutant plants decreases after the endosperm is depleted (2). An absence of chlorophyll *b*-binding proteins in the photosynthetic membranes is found in *fch2* mutants (3, 4).

Origin of mutant:

A spontaneous mutant in progeny from the cross Moister (CIho 2799) X California Coast (CIho 6115) (1).

Mutational events:

fch2.c (28-3398 Chlorina, GSHO 107) in Moister/California Coast (1, 7); *fch2.y* (*lg5*, GSHO 294) in CIho 6151 (8); *clo-f2.2800*, *-f2.2807*, *-f2.3613* in Donaria (PI 209784), *-f2.101*, *-f2.102*, *-f2.103*, *-f2.105*, *-f2.107*, *-f2.108*, *-f2.109* in Tron, *-f2.122*, *-f2.123*, *-f2.133* in Bonus (PI 189763) (5, 6).

Mutant used for description and seed stocks:

fch2.c (28-3398, GSHO 107) in Moister/California Coast; *fch2.c* in Bowman (PI 483237)*7 (GSHO 1993, BW358, NGB 20597).

References:

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10. Tsuchiya, T., and R.J. Singh. 1982. Chromosome mapping in barley by means of telotrisomic analysis. *Theor. Appl. Genet.* 61:201-208.
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Prepared:

T. Tsuchiya. 1972. *Barley Genet. Newsl.* 2:183.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:151-152.

BGS 118, Low number of tillers, *Int1*

Stock number: BGS 118
Locus name: Low number of tillers 1
Locus symbol: *Int1*

Previous nomenclature and gene symbolization:

Reduced number of tillers = *rnt* (3).

Intermedium spike-l = *int-l* (2).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 3HL (3); about 30.5 cM distal from the *uzu1* (*uzu 1*) locus (3, 4).

Description:

The tiller number is reduced to 2 to 4 per plant. These tillers are formed soon after seedling emergence; hence, no late-emerging tillers are observed. Culms are thick and stiff and leaves are dark green (3). Spike malformations occur in most environments.

The spike may have irregular rachis internode lengths and is relatively short. The lower portion of the spike appears more dense. Lateral spikelets in two-rowed cultivars are enlarged and have a pointed apex. Plants homozygous for a recessive allele at the *Int1* locus head slightly earlier than normal sibs (2).

Origin of mutant:

A spontaneous mutant in the hybrid Chikurin Ibaragi 2/Miho Hadaka (3).

Mutational events:

Int1.a (GSHO 833) in Mitake (OUJ408) (3); *int-l.81* (NGB 115499, GSHO 1771) in Bonus (PI 189763) (1, 2).

Mutant used for description and seed stocks:

Int1.a (GSHO 833) in Mitake; *int-l.81* (NGB 115499, GSHO 1771) in Bonus; *Int1.a* in Bowman (PI 483237)*8 (GSHO 1984, BW494, NGB 22157); *int-l.81* in Bowman*6 (GSHO 1961, BW428, NGB 22152).

References:

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2. Lundqvist, U., and A. Lundqvist. 1988. Induced intermedium mutants in barley: origin, morphology and inheritance. *Hereditas* 108:13-26.
3. Nonaka, S. 1973. A new type of cultivar, Mitake, with very few in number, but thick and stiff culms. *Barley Genet. Newsl.* 3:45-47.
4. Nonaka, S. 1974. Further information of the *rnt* locus on chromosome 3. *Barley Genet. Newsl.* 4:56-58.

Prepared:

S. Nonaka. 1973. *Barley Genet. Newsl.* 3:120.

Revised:

T. Tsuchiya. 1980. *Barley Genet. Newsl.* 10:113.

J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:153.

BGS 119, Desynapsis 2, *des2*

Stock number: BGS 119
Locus name: Desynapsis 2
Locus symbol: *des2*

Previous nomenclature and gene symbolization:

Desynaptic chromosomes = *ds* (1, 2).

Inheritance:

Monofactorial recessive (1, 2).

Located in chromosome 3H (1, 2).

Description:

Synapsed homologous chromosomes disjoin precociously because of an apparent lack of chiasmata (1). The chromosomes are paired during pachytene and undergo desynapsis during diplotene. The degree of desynapsis is $d = 6.0 \pm 3.3$ with a range from 7 ring bivalents ($d = 0$) to 2 rod bivalents plus 10 univalents ($d = 12$). Lagging chromosomes and micronuclei are observed frequently at telophase I. Microspore tetrads contain an average of 1.8 micronuclei per tetrad and a range of 0 to 7. Ovule fertility is about 1% and highly variable from spike to spike on the same plant (3). The very low fertility trait occurs infrequently in the F_2 progeny from the cross to Bowman, but nearly 1/4 the plants show reduced seed set (about 60%).

Origin of mutant:

An X-ray induced mutant in Husky (Clho 9537) (1).

Mutational events:

des2.b (GSHO 593) in Husky (Clho 9537) (1, 4).

Mutant used for description and seed stocks:

des2.b (GSHO 593) in Husky; *des2.b* in Bowman (PI 483237)*5 (BW238, NGB 22065).

References:

1. Enns, H., and E.N. Larter. 1960. Note on the inheritance of *ds*; a gene governing meiotic chromosome behaviour in barley. Can. J. Plant Sci. 40:570-571.
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Prepared:

J.M. Hernandez-Soriano, R.T. Ramage, and R.F. Eslick. 1973. Barley Genet. Newsl. 3:125.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:154.

BGS 120, Zebra stripe 1, *zeb1*

Stock number: BGS 120
Locus name: Zebra stripe 1
Locus symbol: *zeb1*

Previous nomenclature and gene symbolization:

Zebra stripe = *zb* (1, 4).

Inheritance:

Monofactorial recessive (1).

Located in chromosome 3HL (1, 3, 4); about 7.0 cM proximal from the *uzu1* (*uzu* 1) locus (2).

Description:

Seedlings may have pale green to yellow bands across the leaves when germinated under cold conditions in the field (1). Cold room studies show that development of the mutant phenotype in seedlings can be induced by 10 to 15 days of cold treatment (0 to 1°C) if initiated within one day after wetting of the seed (5). Alternating cold and warm temperatures in the field induce diagnostic symptoms (5).

Origin of mutant:

A radiation induced mutant in Mars (Clho 7015) (1).

Mutational events:

zeb1.a (C3-1, GSHO 1279) in Mars (Clho 7015) (2, 3).

Mutant used for description and seed stocks:

zeb1.a (GSHO 1279) in Mars; *zeb1.a* in Bowman (PI 483237)*3 (GSHO 1964); *zeb1.a* in Bowman*7 (BW930, NGB 22359).

References:

1. Burnham, C.R. 1958. New linkages found. Barley Newsl. 1:44-47.
2. Kasha, K.J., and C.R. Burnham. 1965. The location of interchange breakpoints in barley. I. Linkage studies and map orientation. Can. J. Genet. Cytol. 7:62-77.
3. Kasha, K.J., and G.W.R. Walker. 1960. Several recent barley mutants and their linkages. Can. J. Genet. Cytol. 2:397-415.
4. Singh, R.J., and T. Tsuchiya. 1974. Further information on telotrisomic analysis in barley. Barley Genet. Newsl. 4:66-69.
5. Tsuchiya T., and R.J. Singh. 1974. Identification of zebra (*zb*) stripe character at early seedling stage. Barley Genet. Newsl. 4:96-97.

Prepared:

T. Tsuchiya. 1975. Barley Genet. Newsl. 5:100.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:155.

BGS 121, Reaction to *Puccinia hordei* 3, *Rph3*

Stock number: BGS 121
Locus name: Reaction to *Puccinia hordei* 3 (barley leaf rust)
Locus symbol: *Rph3*

Previous nomenclature and gene symbolization:

- Resistance to *Puccinia anomala* Rostr = *Pa*₁ (2).
- Resistance to *Puccinia hordei* Otth 3 = *Pa*₃ (6).
- Resistance to *Puccinia hordei* Otth 3 = *Rph3c* (7).

Inheritance:

- Monofactorial dominant (7, 9).
- Located in chromosome 7HL (3, 8); about 9.7 cM distal from the *Xnt1* (xantha seedling 1) locus (3); no linkage to the *lks2* (short awn 2) locus was not observed (3).

Description:

The seedling reaction type is 0 - 0;^c with race 4 culture 57-19, and complete dominance is observed in segregating progenies (6).

Origin of mutant:

Natural occurrence in Estate (CIho 3410, PI 57700) (2, 6).

Mutational events:

Rph3.c in Estate (CIho 3410, PI 57700, GSHO 1316) (2, 6); *Rph3.c* in Aim (CIho 3737) (5); *Rph3.c* in Santizo (PI 39505), Baladi 16 (PI 263160), Beecher (PI 263161), and PI 531990 (4); *Rph3.w* in accession PI 466324 of *Hordeum vulgare* subsp. *spontaneum* (1).

Mutant used for description and seed stocks:

Rph3.c in Estate (GSHO 1316); *Rph3.c* in Bowman (PI 483237)*7 (GSHO 1863); *Rph3.c* in Bowman*11 (BW746, PI 643152, NGB 22452); *Rph3.w* from PI 466324 in Bowman*7 (BW747, NGB 33453).

References:

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7. Roane, C.W., and T.M. Starling. 1970. Inheritance of reaction to *Puccinia hordei* in barley. III. Genes in the cultivars Cebada Capa and Franger. *Phytopathology* 60:788-790.
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News. 15:106-107.

Prepared:

C.W. Roane. 1976. Barley Genet. News. 6:121.

Revised:

J.D. Franckowiak and Y. Jin. 1997. Barley Genet. News. 26:156.

BGS 122, Reaction to *Puccinia hordei* 5, *Rph5*

Stock number: BGS 122
Locus name: Reaction to *Puccinia hordei* 5 (barley leaf rust)
Locus symbol: *Rph5*

Previous nomenclature and gene symbolization:

Resistance to *Puccinia hordei* Otth 5 = *Pa*₅ (6, 7).

Resistance to *Puccinia hordei* B = *B* (5).

Resistance to *Puccinia hordei* Otth = *X* (5, 6).

Resistance to *Puccinia hordei* Otth = *Pa*_x (6).

Resistance to *Puccinia hordei* 6 = *Rph6.f* (11).

Inheritance:

Monofactorial incomplete dominant (3, 5, 6).

Located in chromosome 3HS (4, 11); about 7.0 cM distal from *Rph7* (11), about 0.5 cM proximal from RFLP marker CDO549 (11); about 2.5 cM distal from RFLP marker MWG2021 (4).

Description:

Rph5.e in Magnif 102 showed a seedling infection type of 0 - 0;^c with race 4 culture 57-19, and *Rph6.f* from Bolivia had a 0;ⁿ - 1^c seedling infection type with race 4 culture 57-19. (3). Heterozygotes frequently show an intermediate response (type 2 or 3 reaction) to inoculation with pathogenic races, and incomplete dominance is observed in segregating progenies (3, 5, 6). Zhong et al. (11) demonstrated that *Rph5.e* is allelic to the *Rph6.f* gene extracted from Bolivia (PI 36360). *Rph6.f* was identified as a monofactorial dominant, but an allele at the *Rph2* (reaction to *Puccinia hordei* 2) locus is present in the original cultivar Bolivia (PI 36360) (5, 6, 8).

Origin of mutant:

Natural occurrence in Quinn (PI 39401) (6, 10); natural occurrence in Bolivia (PI 36360) (2, 5).

Mutational events:

Rph5.e in Magnif 102 (PI 337140, GSHO 1597) (10), *Rph5.f* (formerly *Rph6.f*) in Bolivia (PI 36360) (11), *Rph5.ai* in Quinn (PI 39401) along with *Rph2.q* (5, 6).

Mutant used for description and seed stocks:

Rph5.e in Malteria Heda*4/Quinn (Magnif 102, GSHO 1597) (10); *Rph5.f* in Bolivia (GSHO 1598); *Rph5.e* in Bowman (PI 483237)*8 (GSHO 1865, BW755, NGB 22461); *Rph5.f* (without an *Rph2* allele) in Bowman*8 (GSHO 2323, PI 643154, BW756, NGB 22462) (1).

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Prepared:

- C.W. Roane. 1976. *Barley Genet. Newsl.* 6:122.
J.D. Franckowiak and Y. Jin. 1997. *Barley Genet. Newsl.* 26:501, as BGS 575, Reaction to *Puccinia hordei* 6, *Rph6*.

Revised:

- J.D. Franckowiak and Y. Jin. 1997. *Barley Genet. Newsl.* 26:157.
J.D. Franckowiak and B.J. Steffenson. 2005. *Barley Genet. Newsl.* 35:188.
J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:224-225.

BGS 123, Reaction to barley yellow dwarf virus 2, *Ryd2*

Stock number: BGS 123
Locus name: Reaction to barley yellow dwarf virus 2 (BYDV)
Locus symbol: *Ryd2*

Previous nomenclature and gene symbolization:

Resistance to BYDV 2 = *Yd2* (2, 4).

Resistance to BYDV 2 = *Ryd2* (3).

Inheritance:

Monofactorial incomplete dominant (2, 4).

Located in chromosome 3HL (5); about 15.9 cM proximal from the *dsp10* (dense spike 10) locus (5).

Description:

Plants show an intermediate reaction to BYDV that limits expression of dwarfing and yellow discoloration of leaves (3, 4). Plants with the *Ryd2.b* gene show less yield and seed size reduction when infected with BYDV and under drought and heat stress.

Origin of mutant:

Natural occurrence in Clho 1227, Clho 1237, Clho 2376, and Clho 14119 (four accessions from Ethiopia) (4, 5).

Mutational events:

Ryd2.b in Clho 1227, Clho 1237, Clho 2376, and Clho 14119 (3, 5); *Ryd2.c* in Chikurin Ibaraki 1 (Clho 7370, GSHO 783) (susceptible to isolate 2t) (1).

Mutant used for description and seed stocks:

Ryd2.b in Abyssinian (Clho 2376, GSHO 1315); *Ryd2.b* from Clho 2376 in Bowman (PI 483237)*7 (GSHO 1969); *Ryd2.b* from Clho 2376 in Glenn (Clho 15769)*8 (GSHO 2370). (Presence of *Ryd2* in the Bowman and Glenn lines has not been confirmed).

References:

1. Chalhoub, B.A., A. Sarafi, and H.D. Lapierre. 1995. Partial resistance in the barley (*Hordeum vulgare* L.) cultivar 'Chikurin Ibaraki 1' to two PAV-like isolates of barley yellow-dwarf virus: allele variability at the *Yd2* gene locus. *Plant Breed.* 114:303-307.
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Prepared:

C.W. Schaller. 1976. *Barley Genet. Newsl.* 6:123.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:158.

BGS 124, Six-rowed spike 4, *vrs4*

Stock number: BGS 124
Locus name: Six-rowed spike 4
Locus symbol: *vrs4*

Previous nomenclature and gene symbolization:

Multiflorus = *mul* (8, 17).
Intermedium spike-e = *int-e* (6, 11).
Six-rowed spike 4 = *v4* (3).

Inheritance:

Monofactorial recessive (3, 4, 5, 7).
Located in chromosome 3HL (5, 14, 15, 16); about 27.5 cM from the *uzu1* (*uzu* 1) locus (5); *int-e.58* is associated with SNP markers 1_0672 to 2_1083 (positions 38.56 to 156.06 cM) in 3H bins 04 to 10 of the Bowman backcross-derived line BW423 (1); *mul1.a* is associated with SNP markers 1_0762 and 2_0115 (positions 38.56 and 126.83 cM) in 3H bins 04 and 08 of line BW606 (1); *vrs4.k* is associated with SNP markers 1_0863 to 1_0926 (positions 64.85 to 85.26 cM) in 3H bin 05 and with SNP markers 2_1493 to 1_1330 (positions 161.43 to 178.12 cM) in 3H bin 10 of the Bowman backcross-derived line BW903 (1); the lack of SNP marker heterogeneities in the centromeric region of the BW lines and more markers retained in 3HS indicate that the *vrs4* locus is more markers retained in 3HS indicate that the *vrs4* locus is more likely in 3H bin 05 (1, 2).

Description:

Alleles at this locus enhance the development of lateral spikelets and formation of additional spikelets to various degrees. The *int-e* mutants, which were isolated in two-rowed cultivars, have enlarged lateral spikelets that may set seed in the upper two-thirds of the spike. Kernels in lateral spikelets are smaller than those from central spikelets in *int-e* mutants. The rachilla may be deformed by partial formation of an extra spikelet. The awn size on lateral spikelets ranges from a pointed apex to 3/4 normal length (12). The *mul1.a* and *vrs4.k* alleles, which were isolated in six-rowed cultivars, may produce numerous extra spikelets at the base of the lateral spikelets and on the rachilla (4, 8). Plants of the backcross derived line BW903 with the *vrs4.k* allele and BW606 with *mu1.a* are slightly taller than Bowman, plants lodge easily, and rachis internodes are slightly longer. Kernels of BW423 with *int-e.58* had weights that range similar to those of Bowman to 10% less. Kernels of BW606 and BW903, which include small lateral ones, had average weights 20 to 40% less than those of Bowman. The kernel weights for BW606 were slightly less than those of BW093. Kernels of all BW lines with *vrs4* alleles are about 10% shorter than those of Bowman (2).

Origin of mutant:

A gamma-ray induced mutant in MFB 104 (PI 232921) (5).

Mutational events:

mul1.a (Alb Acc 321, GSHO 561) in Montcalm (Clho 7149) (8, 17); *vrs4.k* (Gamma III 3B, MFB-2, GSHO 775) in MFB 104 (PI 232921), *vrs4.l* (Xc 41.5, Piro-2) in Pirolina (PI 262210) (5); *vrs4.m* (X17 2497, Piro-7) in Pirolina (4, 5); *int-e.4* (trans) (NGB 115212) in Bonus (PI 189763), -e.20 (trans) (NGB 115438), -e.23 (NGB 115441), -e.26 (NGB 115444) in Foma (Clho 11333), -e.58 (NGB 115476, GSHO 1776), -e.66 (NGB 115484) in Kristina (NGB 1500), -e.65 (NGB 115438) in Bonus (11); *int-e.72* (NGB 115490), -e.87 (NGB 115505) in Bonus, -e.89 (NGB 115507), -e.90 (NGB 115508), -e.91 (NGB 115509), -e.92 (NGB 115510), -e.101 (NGB 115519) in Hege (10); *hex-v.46* (NGB 115583), *hex-v.47* (NGB 115584), *hex-v.48* (NGB 115585) (9, 10).

Mutant used for description and seed stocks:

vrs4.k (Gamma III 3B, GSHO 775) in MFB 104; *int-e.58* in Kristina (GSHO 1776, NGB 115476); *mul1.a* in Bowman (PI 483237)*6 (GSHO 1985); *mul1.a* in Bowman*7 (BW606, NGB 22172); *vrs4.k* in Bowman*6 (GSHO 1986); *vrs4.k* in Bowman*7 (BW903, NGB 22335); *int-e.58* in Bowman*6 (GSHO 1987); *int-e.58* in Bowman*7 (BW423, NGB 20658).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:159-160.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:101-102.

BGS 125, Lazy dwarf 1, *lzd1*

Stock number: BGS 125
Locus name: Lazy dwarf 1
Locus symbol: *lzd1*

Previous nomenclature and gene symbolization:

Dwarf 4 = *dw4* (1).

Inheritance:

Monofactorial recessive (2, 4).

Located in chromosome 3HS (3, 4); over 16.3 cM distal from the *alm1* (albino lemma 1) locus (3, 4).

Description:

Plants have a very procumbent growth habit prior to the boot stage. Plants are 3/4 normal height, maturity is delayed, and seedlings are very responsive to gibberellic acid (2, 4). In the Bowman backcross-derived line, leaves are wider and shorter than in the recurrent parent.

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (1).

Mutational events:

lzd1.a (OUM005, GSHO 1787) in Akashinriki (OUJ659, PI 467400) (2, 4).

Mutant used for description and seed stocks:

lzd1.a (GSHO 1787) in Akashinriki; *lzd1.a* in Bowman (PI 483237)*8 (GSHO 1938, BW499, NGB 20727).

References:

1. Konishi, T. 1970. Studies on EMS-induced mutation in barley III. Nogaku Kenkyu 53:141-152.
2. Konishi, T. 1975. Characteristics and inheritance of EMS-induced mutants in barley. Nogaku Kenkyu 55:53-56.
3. Konishi, T., J. Hayashi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley. VII. Location of six new mutant genes on chromosome 3. Ber. Ohara Inst. landw. Biol., Okayama Univ. 18:251-264.
4. Takahashi, R., J. Hayashi, T. Konishi, and I. Moriya. 1975. Linkage analysis of barley mutants. Barley Genet. Newsl. 5:56-60.

Prepared:

T. Konishi and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:161.

BGS 126, Slender dwarf 1, *sld1*

Stock number: BGS 126
Locus name: Slender dwarf 1
Locus symbol: *sld1*

Previous nomenclature and gene symbolization:

Dwarf 1 = *dw1* (3).

Light green dwarf = *dw-1* (8).

Inheritance:

Monofactorial recessive (4, 9).

Located in chromosome 3HL (6, 8, 9); over 6.3 cM distal from the *uzu1* (*uzu 1*) locus (6, 8); about 20.5 cM distal from the *uzu1* locus (8); about 1.2 cM from AFLP marker E3634-8 in subgroup 27 of the Proctor/Nudinka map (7); *sld1.a* is associated with SNP markers 2_1402 to 2_0362 (positions 77.00 to 119.10 cM) in 3H bins 05 to 07 of the Bowman backcross-derived line BW859 (1); *sld1.a* with *uzu1.a* is associated with SNP markers 1_0653 to 2_0115 (positions 92.55 to 126.83 cM) in 3H bins 06 to 08 of the Bowman backcross-derived line BW860 (1); *sld1.c* is associated with SNP markers 2_1145 to 2_0093 (positions 65.96 to 127.91 cM) in 3H bins 05 to 08 of the Bowman backcross-derived line BW861 (1); BW859 and BW860 have a common SNP patterns from 2_0017 to 2_0362 (positions 106.46 to 119.10 cM) in 3H bin 07 (1), in 3H bin 07.

Description:

Plant height is reduced to about 1/2 to 2/3 of normal, plant development is delayed, and plants are slightly yellow green in color (3, 8). Plants of the mutant *sld1.a* (*dw-a*, OUM148) headed 4 days later and were shorter, 81 vs. 122 cm, than their parent, Akashinriki (5). Kernel weights and kernels per spike of *sld1.a* plants were reduced and grain yields were 30% lower (5). The distribution of leaves in *sld1* plants was altered because the peduncle is relatively long in proportion to the other internodes. Plants homozygous for the *sld1.c* allele were slightly weaker and shorter than *sld1.a* plants in their respective Bowman backcross-derived lines, BW861 and BW859 (2). Heading was delayed about 5 days in both BW859 and BW861. BW859 plants exhibited about 30% reduction in plant height, but had about 3 more kernels per spike. Kernel weights for BW859 were 5 to 15% lower than those of Bowman and grain yields ranged from 1/3 to 90% those of Bowman. Plants of BW861 showed a 40% reduction in plant height compared to Bowman, spikes had an average of 2 more kernels, kernel weights were 10 to 25% lower, and grain yield ranged from 10 to 75% those of Bowman (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (3).

Mutational events:

sld1.a (*dw-a*, OUM148, GSHO 2488) in Akashinriki (OUJ659, PI 467400) (3, 6); *sld1.c* (862PK, GSHO 2489) in Plena (PI 321822) (2, 8).

Mutant used for description and seed stocks:

sld1.a in Akashinriki (GSHO 2488, OUM148); *sld1.a* in Bowman (PI 483237)*7 (GSHO 1970); *sld1.a* in Bowman*8 (BW859, NGB 22296); *sld1.c* in Bowman*7 (GSHO 1972, BW861, NGB 22298); *sld1.a* with *uzu1.a* (OUM148, GSHO 2489) from Akashinriki in Bowman*8 (GSHO 1971, BW860, NGB 22297).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).

3. Konishi, T. 1970. Studies on EMS-induced mutation in barley III. *Nogaku Kenkyu* 53:141-152.
4. Konishi, T. 1975. Characteristics and inheritance of EMS-induced mutants in barley. *Nogaku Kenkyu* 55:53-56.
5. Konishi, T. 1976. The nature and characteristics of EMS-induced dwarf mutants in barley. p. 181-189. *In* H. Gaul (ed.). *Barley Genetics III. Proc. Third Int. Barley Genet. Symp.*, Garching, 7-12 July 1975. Verlag Karl Thiemig, München.
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8. Szarejko, I., and M. Maluszynski. 1984. Two new dwarfism genes on barley chromosome 3. *Barley Genet. Newsl.* 14:35-38.
9. Takahashi, R., J. Hayashi, T. Konishi, and I. Moriya. 1975. Linkage analysis of barley mutants. *Barley Genet. Newsl.* 5:56-60.

Prepared:

T. Konishi and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:162.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:103-104.

BGS127, Pubescent leaf blade 1, *Pub1*

Stock number: BGS 127
Locus name: Pubescent leaf blade 1
Locus symbol: *Pub1*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial dominant (2).
Located in chromosome 3HL (1).

Description:
Both the upper and lower surface of the leaf blade have widely scattered, short (1 to 2 mm) hairs. The hairs tend to be aligned along the smaller leaf veins. The hairs are more difficult to observe on older leaves or plants grown in the field. Some accessions of *Hordeum vulgare* subsp *spontaneum* have numerous short hairs on both surfaces of the leaf.

Origin of mutant:
Natural occurrence in Steptoe (CIho 15229) (1), and in many accessions of *Hordeum vulgare* subsp *spontaneum*.

Mutational events:
Pub1.a in R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 1580) (2); *Pub1.a* in Steptoe (1).

Mutant used for description and seed stocks:
Pub1.a in Steptoe (GSHO 1576); *Pub1.a* from R.I. Wolfe's Multiple Dominant Marker Stock in Bowman (PI 483237)*6 (GSHO 1976); *Pub1.a* from R.I. Wolfe's Multiple Dominant Marker Stock in Bowman*7 (BW 650, NGB 22215).

References:
1. Kleinhofs, A., A. Killian, M.A. Saghai Maroof, R.M. Biyashev, P. Hayes, F.Q. Chen, N. Lapitan, A. Fenwick, T.K. Blake, V. Kanazin, E. Ananiev, L. Dahleen, D. Kudrna, J. Bollinger, S.J. Knapp, B. Liu, M. Sorrells, M. Heun, J.D. Franckowiak, D. Hoffman, R. Skadsen, and B.J. Steffenson. 1993. A molecular, isozyme and morphological map of the barley (*Hordeum vulgare*) genome. Theor. Appl. Genet. 86:705-712.
2. Wolfe, R.I., and J.D. Franckowiak. 1991. Multiple dominant and recessive marker stocks in spring barley. Barley Genet. Newsl. 20:117-121.

Prepared:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:163.

BGS 128, Short crooked awn 1, *sca1*

Stock number: BGS 128
Locus name: Short crooked awn 1
Locus symbol: *sca1*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (2).
Located in chromosome 3HS (2); about 1.4 cM distal from the *alm1* (albino lemma 1) locus (1, 2).

Description:
In the original stock, awns are reduced to a length of only 2 cm and are curved outward at the tip (3). Awn tips may have a stigma-like appearance in the original stock. In the Bowman backcross-derived line, awns are short (less than 1/4 normal), but awn tips are not curved or stigma-like.

Origin of mutant:
An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (2).

Mutational events:
sca1.a (OUM206, GSHO 2439) in Akashinriki (OUJ659, PI 467400) (1, 2).

Mutant used for description and seed stocks:
sca1.a in Akashinriki (GSHO 2439), *sca1.a* in Bowman (PI 483237)*6 (GSHO 1951);
sca1.a in Bowman*8 (BW769, NGB 22237).

References:
1. Konishi, T., J. Hayashi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley. VII. Location of six new mutant genes on chromosome 3. Ber. Ohara Inst. landw., Biol. Okayama Univ. 18:251-264.
2. Moriya, I., and R. Takahashi. 1980. Linkage studies of three barley mutants. Barley Genet. Newsl. 10:47-51.

Prepared:
J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:164.

BGS 129, White streak 6, *wst6*

Stock number: BGS 129
Locus name: White streak 6
Locus symbol: *wst6*

Previous nomenclature and gene symbolization:

White stripe j = *wst_j* (5).

Inheritance:

Monofactorial recessive (5).

Located in chromosome 3HL (4, 5); about 10.6 cM distal from the *uzu1* (*uzu 1*) locus (3, 4, 5); *wst6.j* is associated with SNP markers 2_1305 to 2_0626 (positions 103.33 to 152.84 cM) in 3H bins 06 to 10 of the Bowman backcross-derived line BW915 (1), likely in 3H bin 07.

Description:

When grown under low temperature conditions, the leaf sheath and leaf blade become whitish or white streaked. In some cases, only the leaf tip and the central portion of the blade remained green (5). White streaks were not expressed above 20°C (5). A white streaked phenotype was expressed in seedlings grown under greenhouse conditions (2). Plants of BW915, the Bowman backcross-derived line for *wst6.j*, were up to 7 days later, 10 to 15 cm shorter, and lower yielding than Bowman in some environments. However, BW915 was similar Bowman in other field trials (2).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (5).

Mutational events:

wst6.j (OUM231, GSHO 2500) in Akashinriki (OUJ659, PI 467400) (4, 5).

Mutant used for description and seed stocks:

wst6.j (OUM231, GSHO 2500) in Akashinriki; *wst6.j* plus *uzu1.a* in Bowman (PI 483237)*3 (GSHO 1968); *wst6.j* in Bowman*7 (BW915, NGB 22346).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Konishi, T., J. Hayashi, I. Moriya, and R. Takahashi. 1984. Inheritance and linkage studies in barley. VII. Location of six new mutant genes on chromosome 3. *Ber. Ohara Inst. landw. Biol., Okayama Univ.* 18:251-264.
4. Moriya, I., and R. Takahashi. 1980. Linkage studies of three barley mutants. *Barley Genet. Newsl.* 10:47-51.
5. Takahashi, R., J. Hayashi, and I. Moriya. 1974. New linkage data obtained during 1972-73 season. *Barley Genet. Newsl.* 4:74-76

Prepared:

J.D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:165.

Revised:

J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:105.

BGS 130, Early maturity 10, *eam10*

Stock number: BGS 130
Locus name: Early maturity 10
Locus symbol: *eam10*

Previous nomenclature and gene symbolization:

Early maturity sp = *ea_{sp}* (8).

Inheritance:

Monofactorial recessive (8).

Located in chromosome 3HL (8); about 2.0 ± 5.8 cM from the *Est1-Est4* (esterase 1, esterase 4) locus (8); about 5.8 cM distal from RFLP marker Xmwg546 (1).

Description:

In winter nurseries at Ciudad Obregón, Sonora, Mexico and Davis, California, USA, plants of Super Precoz 2H head about 11 days earlier than lines with the genes *eam7.g* or *eam8.k* for photoperiod insensitivity from Atsel and Sv Mari, respectively (8). The *eam10.m* gene appears to suppress expression of the *eam7.g* and *eam8.k* genes (8). Plants expressing *eam10.m* become chlorotic (yellow green) under photothermal stress. Zeaxanthin increases at the expense of chlorophyll and other pigments (7). The chlorotic appearance is similar to that observed in plants homozygous for other recessive genes for early maturity (*eam7*, *eam8*, and *eam9*) (2, 5, 7). Plants in the Bowman *eam10.m* line head two days earlier than Bowman under long days and are slightly shorter (5).

Origin of mutant:

Present in Super Precoz 2H (PI 527381) from Russia (7), but originating probably as an induced mutant in MC20 (3, 4, 7).

Mutational events:

eam10.m (GSHO 2504) in Super Precoz 2H (PI 527381) plus a dominant maturity enhancer (4, 5, 7); *eam10.m* in Amber Nude (GSHO 2505) without the enhancer (4).

Mutant used for description and seed stocks:

eam10.m in Super Precoz 2H (GSHO 2504); *eam10.m* in Amber Nude (GSHO 2505); *eam10.m* from Super Precoz in Bowman (PI 483237)*4 (GSHO 3421); *eam10.m* from Super Precoz in Bowman*5 (BW284, NGB 20568).

References:

1. Börner, A., G.H. Buck-Sorlin, P.M. Hayes, S. Malyshev, and V. Korzun. 2002. Molecular mapping of major genes and quantitative trait loci determining flowering time in response to photoperiod in barley. *Plant Breed.* 121:129-132.
2. Dormling, I., and Å. Gustafsson. 1969. Phytotron cultivation of early barley mutants. *Theor. Appl. Genet.* 39:51-61.
3. Favret, E.A. 1972. El mejoramiento de las plantas por inducción de mutaciones en latinoamerica. p. 49-59. *In* Induced Mutations and Plant Improvement. Int. Atomic Energy Agency, Vienna.
4. Favret, E.A., and G.S. Ryan. 1966. New useful mutants in plant breeding. p. 49-61. *In* Mutations in Plant Breeding. Int. Atomic Energy Agency, Vienna.
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7. Gallagher, L.W., A.A. Hafez, S.S. Goyal, and D.W. Rains. 1994. Nuclear mutations affecting chloroplastic pigments of photoperiod-insensitive barley. *Plant Breed.* 113:65-70.
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Prepared:

- L.W. Gallagher and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:166.
Revised:
J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:226-227.

BGS 131, Granum-a, *gra-a*

Stock number: BGS 131
Locus name: Granum-a
Locus symbol: *gra-a*

Previous nomenclature and gene symbolization:

Granum-a = *gran-a* (2).

Inheritance:

Monofactorial recessive (2, 6).

Located in chromosome 7H (1); *gra-a.1* is associated with SNP markers 1_0861 to 1_0078 (positions 183.90 to 187.83 cM) in 7H bin 11 of the Bowman backcross-derived line BW398 (1); *gra-a.2* is associated with SNP markers 1_0078 to 1_0547 (position 187.83 to 231.00 cM) in 7H bin 11 to 13 of the Bowman backcross-derived line BW399 (1), likely in 7H bin 11. Previously the *gra-a* locus was reported to be in 3HL (2, 7).

Description:

Plants have numerous, thin tillers with narrow leaves and short internodes (1/2 normal plant height). Spikes are less than half normal length and seeds are thin and small (2, 6). Spikes emerge from the sheath of the flag leaf prematurely, 4 to 7 days before anthesis (4). Compared to Bowman plants of Bowman backcross-derived lines BW398 and 399 were about half of normal height and peduncles were about 1/3 normal length. Awns and rachis internodes of the *gra-a* spikes were slightly shorter than those of Bowman. The tip of the spike has a fasciated appearance because spikelets are very close together. The number of kernels per spike for BW398 and BW299 plants were often 4 to 7 less than for Bowman. Kernel weights about 25% less than those of Bowman, but grain yields were almost normal (3).

Origin of mutant:

An X-ray induced mutant in Donaria (PI 161974) (2, 6).

Mutational events:

gra-a.1 (GSHO 1757) in Donaria (PI 161974) (2, 6); *gra-a.2* (GSHO 1758) from a Tokak (PI 178421) mutant in OR-SS-2 (4, 5, 7); *gra-a.3* (DWS1176) in HE2816 (likely from HE-MN-C 292) from Milan Váša (4, 5).

Mutant used for description and seed stocks:

gra-a.1 (GSHO 1757) in Donaria; *gra-a.1* in Bowman (PI 483237)*7 (GSHO 1980, BW398, NGB 20635); *gra-a.2* in Bowman*7 (GSHO 1981, BW 399, NGB 20636).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. *Plant Physiology* 155:617-627.
2. Fischbeck, G., and H. Häuser. 1976. Research notes. *Barley Genet. Newsl.* 6:28-29.
3. Franckowiak, J.D. (Unpublished).
4. Franckowiak, J.D. 1992. Allelism tests among selected semidwarf barleys. *Barley Genet. Newsl.* 21:17-23.
5. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes: A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
6. Häuser, J., and G. Fischbeck. 1976. Untersuchungen zur Lokalisierung einiger Mutationen von Gerste (*Hordeum sativum*). *Z. Pflanzenzücht.* 77:269-280.
7. Sears, R.G., W.E. Kronstad, and R.J. Metzger. 1981. Inheritance of dwarf and semidwarf plant height in barley. *Crop Sci.* 21:828-833.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:167.
Revised:
J.D. Franckowiak. 2012. Barley Genet. Newsl. 42:216-217.

BGS 132, *Breviaristatum-a*, *ari-a*

Stock number: BGS 132
Locus name: *Breviaristatum-a*
Locus symbol: *ari-a*

Previous nomenclature and gene symbolization:

Breviaristatum-6 = *ari-6* (3, 4).
Short awn 7 = *lk7* (9).

Inheritance:

Monofactorial recessive (4).
Located in chromosome 3HS (6, 7, 8); probably less than 2.4 cM from the centromere (7); *ari-a.6* is associated with SNP markers 2_1197 to 1_0653 (positions 78.82 to 92.55 cM) in 3H bins 05 to 06 of the Bowman backcross-derived line BW038 (1), likely in 3H bin 05.

Description:

A common feature of mutants at this locus is instability in the expression of awn length, ranging from very short to 5/6 normal length in various environments (4). In some environments, secondary or tertiary tillers may show a drastic reduction in the length of stem internodes, spikes, and awns. Awns are thin and brittle and may flare somewhat on later tillers. Kernels are thin with fine wrinkles on the lemma (4). Plants of BW038, the Bowman backcross-derived line for mutant *ari-a.6*, were 10 to 20% shorter than Bowman and their awns extended beyond the tip of the spike 5 to 9 cm vs. 11 to 12 cm for Bowman. Kernels of BW038 were slightly smaller in size and weighed 10 to 20% less than the Bowman kernels. Grain yields of BW038 were about 2/3 those of Bowman (2).

Origin of mutant:

A gamma-ray induced mutant in Bonus (PI 189763) (4).

Mutational events:

ari-a.6 (NGB 115850, GSHO 1648), *-a.7* (NGB 115851) in Bonus (4); *ari-a.8* (NGB 115852), *-a.23* (NGB 115871) in Bonus (5); *ari-a.26* (NGB 115874) in Bonus (4); *ari-a.31* (NGB 115880) in Bonus (5); *ari-a.37* (NGB 115887), *-a.48* (NGB 115900) in Bonus, *-a.118* (NGB 115930), *-a.121* (NGB 115933), *-a.124* (NGB 115936), *-a.126* (NGB 115938) in Foma (Clho 11333) (4); *ari-a.122* (NGB 115934), *-a.125* (NGB 115937), *-a.148* (NGB 115960) in Foma (5); *ari-a.152* (NGB 115962), *-a.162* (NGB 115972), *-a.174* (NGB 115984), *-a.211* (NGB 116020) in Foma (4); *ari-a.216* (NGB 116025) in Foma (5); *ari-a.273* (NGB 116085), *-a.277* (NGB 116090), *-a.279* (NGB 116092), *-a.287* (NGB 116104), *-a.293* (NGB 116113) in Kristina (NGB 1500) (4); *ari-a.296* (NGB 116116), *-a.305* (NGB 116131) in Kristina (5); *lks7.i* (Kmut 114) in Asahi 5 (OUJ509) (9).

Mutant used for description and seed stocks:

ari-a.6 in Bonus (GSHO 1648, NGB 115850); *ari-a.6* in Bowman (PI 483237)*7 (GSHO 1958, BW038, NGB 20466).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
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7. Persson, G. 1969. An attempt to find suitable genetic markers for the dense ear loci in barley II. *Hereditas* 63:1-28.
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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:168.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:106.

BGS 133, Semidwarf 2, *sdw2*

Stock number: BGS 133
Locus name: Semidwarf 2
Locus symbol: *sdw2*

Previous nomenclature and gene symbolization:

Semidwarf-b = *sdw-b* (1).

Inheritance:

Monofactorial recessive (1).

Located in chromosome 3HL (1); over 34.5 cM distal from the *sl/d1* (slender dwarf 1) locus (1).

Description:

Plants are about 3/4 normal height; culms are thin with narrow, short, erect leaves. The flag leaf is narrow and short. The peduncle is short, the collar has a small leaf-like bract, and the basal rachis internode is elongated (1).

Origin of mutant:

A N-methyl-N-nitrosourea induced mutant in Mg4170 (1).

Mutational events:

sdw2.b (267MK, later called 437MK, GSHO 2466) in Mg4170 (1).

Mutant used for description and seed stocks:

sdw2.b (GSHO 2466) in Mg4170; *sdw2.b* in Bowman (PI 483237)*7 (GSHO 1965, BW829, NGB 22266).

References:

1. Szarejko, I., and M. Maluszynski. 1984. Two new dwarfism genes on barley chromosome 3. Barley Genet. Newsl. 14:35-38.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:169.

BGS 134, Erectoides-c, *ert-c*

Stock number: BGS 134
Locus name: Erectoides-c
Locus symbol: *ert-c*

Previous nomenclature and gene symbolization:

Erectoides-1 = *ert-1* (4).

Inheritance:

Monofactorial recessive (7, 8).

Located in chromosome 3HL (6, 12, 13); about 3.7 cM from the centromere (10, 11); about 2.9 cM proximal from the *msg5* (male sterile genetic 5) locus (2); *ert-c.1* is associated with SNP markers 1_0380 to 2_1513 (positions 78.82 to 166.78 cM) in 3H bins 05 to 10 and with SNP markers 1_1302 to 2_1110 (positions 86.79 to 109.78 cM) in 2H bins 07 to 08 of the Bowman backcross-derived line BW305 (1).

Description:

Spikes have a compact or semicompact appearance caused by a reduction in rachis internode length, with values from 1.7 to 2.9 mm (5, 12). The spike has a pyramid shape with shorter rachis internodes at the base and longer ones near the apex. The culm length is also highly variable among mutants at the *ert-c* locus. Mutants *ert-c.66* and *ert-c.153* are partially sterile, much shorter in culm length, and have a more bushy growth pattern than other mutants at this locus (5, 12). GA₃ treatment of plants as the flag leaf emerges decreases spike density (14). The Bowman backcross-derived line for *ert-c.1* (BW305) has a translocation between 2HL and 3HL based on retained SNP markers (1). Plants of BW305 were slightly later and taller than Bowman plants. Rachis internode lengths for BW305 averaged 3.4 vs. 4.6 mm and spikes had 5 to 7 more fertile rachis internodes (3). Compared to Bowman, BW305 had similar kernel weights and grain yields (3).

Origin of mutant:

An X-ray induced mutant in Gull (CIho 1145, GSHO 466) (4, 7, 8).

Mutational events:

ert-c.1 (trans) (NGB 112605, GSHO 471) in Gull (CIho 1145, GSHO 466) (7, 15); *ert-c.14* (trans) (NGB 112615, GSHO 473) in Maja (PI 184884), -c.39 (NGB 112639), -c.47 (trans) (NGB 112646), -c.48 (NGB 112647), -c.59 (trans) (NGB 112658), -c.62 (NGB 112661), -c.66 (NGB 112665), -c.70 (trans) (NGB 112669), -c.75 (NGB 112674) (trans), -c.82 (NGB 112681), -c.83 (NGB 112682), -c.85 (NGB 112684), -c.88 (NGB 112687) in Bonus (PI 189763) (7); *ert-c.91* (NGB 112690), -c.95 (NGB 112694), -c.97 (NGB 112696), -c.98 (NGB 112697), -c.108 (NGB 112707), -c.137 (NGB 112736), -c.153 (NGB 112752), -c.173 (NGB 112774), -c.177 (NGB 112778) in Bonus (12); *ert-c.176* (NGB 112777), -c.179 (NGB 112780), -c.188 (NGB 112789) in Bonus (9); *ert-c.310* (NGB 112826), -c.311 (NGB 112827), -c.312 (NGB 112828) in Foma (CIho 11333) (12); *ert-c.320* (NGB 112835) in Foma (9); *ert-c.327* (NGB 112842), -c.342 (NGB 112858), -c.351 (NGB 112867) in Foma (12); *ert-c.352* (NGB 112868) in Foma (9); *ert-c.355* (NGB 112871), -c.369 (NGB 112885), -c.386 (NGB 112901), -c.395 (NGB 112912) in Foma (12); *ert-c.463* (NGB 112978) in Foma (9); *ert-c.495* (NGB 113011) in Foma (12).

Mutant used for description and seed stocks:

ert-c.1 in Gull (GSHO 471, NGB 112605); *ert-c.1* in Bowman (PI 483237)*7 (GSHO 1960, BW305, NGB 20587).

References:

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12. Persson, G., and A. Hagberg. 1969. Induced variation in a quantitative character in barley. Morphology and cytogenetics of *erectoides* mutants. *Hereditas* 61:115-178.
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14. Stoy, V., and A. Hagberg. 1967. Effects of growth regulators on ear density mutants in barley. *Hereditas* 58:359-384.
15. Tjio, J.H., and A. Hagberg. 1951. Cytological studies on some X-ray mutants in barley. *Anales Estac. Exp. Aula Dei* 2:149-167.

Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:170-171.

Revised:

U. Lundqvist and J.D. Franckowiak. 2011. *Barley Genet. Newsl.* 41:108-109.

BGS 135, Erectoides-ii, *ert-ii*

Stock number: BGS 135
Locus name: Erectoides-ii
Locus symbol: *ert-ii*

Previous nomenclature and gene symbolization:

Erectoides-79 = *ert-79* (1).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 3HL (2, 3); over 6.6 cM distal from the centromere (2, 3).

Description:

Plants are about 1/2 normal height and the spike has an elongated basal rachis internode. Spikes are relatively short and show a slight reduction in rachis internode length with a range of values from 2.7 to 3.0 mm (4).

Origin of mutant:

An X-ray induced mutant in Bonus (PI 189763) (1).

Mutational events:

ert-ii.79 (NGB 112678, GSHO 483) in Bonus (PI 189763) (1, 4).

Mutant used for description and seed stocks:

ert-ii.79 in Bonus (NGB 112678, GSHO 483); *ert-ii.79* in Bowman (PI 483237)*7 (GSHO 1982, BW312, NGB 22108).

References:

1. Hagberg, A., G. Persson, and A. Wiberg. 1963. Induced mutations in the improvement of self-pollinated crops. p. 105-124. *In* E. Åkerberg and A. Hagberg (eds.) Recent Plant Breeding Research. Svalöf 1946-1961. Almqvist & Wiksell, Stockholm.
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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:172.

BGS 136, Reaction to *Puccinia hordei* 7, *Rph7*

Stock number: BGS 136
Locus name: Reaction to *Puccinia hordei* 7 (barley leaf rust)
Locus symbol: *Rph7*

Previous nomenclature and gene symbolization:

Resistance to *Puccinia hordei* Otth y = *Pay* (7).
Resistance to *Puccinia hordei* Otth 5 = *Pa₅* (10).
Resistance to *Puccinia hordei* Otth 7 = *Pa7* (8).

Inheritance:

Monofactorial dominant (7, 10).
Located in chromosome 3HS (14, 15); linkage to markers in the centromeric region was reported (11); about 24.0 cM from the *ant17* (proanthocyanidin-free 17) locus (5); about 1.3 cM distal from RFLP marker cMWG691 in 3H bin 01 (6); about 3.2 cM from receptor-like kinase gene *Hv3Lrk* (2); about 7.0 cM proximal from *Rph5* locus (16).

Description:

The seedling reaction type is 0;ⁿ - 1^c (4, 11). Temperature studies show that resistance conferred by the *Rph7.g* gene is not expressed well above 20°C (4, 15). Cebada Capa is indistinguishable from the cultivar Forrajera Klein (possibly identical to PI 331904) (1). The *Rph7* regions from Morex (*rph7*) and Cebada Capa (*Rph7*) were sequenced and compared to similar regions from 39 other cultivars. The data suggest that a large amount of haplotype variability exists in the cultivated barley gene pool and indicate rapid and recent divergence at this locus (12).

Origin of mutant:

Natural occurrence in Cebada Capa (PI 53911) (7, 8, 10).

Mutational events:

Rph7.g in Cebada Capa (PI 53911) (7, 8, 10); *Rph7.g* in France 7 and France 21 (7); *Rph7.g* in Dabat, Gondar (PI 199964), and La Estanzuela (9, 13, 16); *Rph7.ac* in Tu17a, a Bowman backcross-derived line from Tunisia 17 (3).

Mutant used for description and seed stocks:

Rph7.g in Cebada Capa (GSHO 1318); *Rph7.g* in Bowman (PI 483237)*8 (GSHO 1994, PI 643156, BW758, NGB 22464), *Rph7.ac* (Tu17a) from Tunisia 17 in Bowman*6 (GSHO 2328); *Rph7.ac* (in Bowman*8 (BW757, NGB 22463)).

References:

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Prepared:

J.D. Franckowiak and Y. Jin. 1997. Barley Genet. Newsl. 26:173.

Revised:

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:228-229.

BGS 137, Reaction to *Puccinia hordei* 10, *Rph10*

Stock number: BGS 137
Locus name: Reaction to *Puccinia hordei* 10 (barley leaf rust)
Locus symbol: *Rph10*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial dominant (1).

Located in chromosome 3HL (1); about 15.0 cM from the *Est2* (esterase 2) locus (1).

Description:

The seedling reaction varies from a necrotic fleck to a moderate sized uredinium, and heterozygotes have an intermediate reaction (1). Leaf rust culture Aust 220 from Australia is used to detect resistance in allelism tests and backcross-derived progenies.

Origin of mutant:

Natural occurrence in accession 'Bar Giyyora 30' of *Hordeum vulgare* subsp. *spontaneum*, but isolated in a Clipper backcross-derived line (1).

Mutational events:

Rph10.o (Clipper BC8, GSHO 1588) from *Hordeum vulgare* subsp. *spontaneum* in Clipper*4/Bar Giyyora 30 called BC8 (1).

Mutant used for description and seed stocks:

Rph10.o (BC8, GSHO 1588) in Clipper*4/Bar Giyyora 30; *Rph10.o* in Bowman (PI 483237)*2 (GSHO 1995); *Rph10.o* in Bowman*6 (PI 643159, BW683, NGB 22389).

References:

1. Feuerstein, U., A.H.D. Brown, and J.J. Burdon. 1990. Linkage of rust resistance genes from wild barley (*Hordeum spontaneum*) with isozyme markers. Plant Breed. 104:318-324.

Prepared:

J.D. Franckowiak and Y. Jin. 1997. Barley Genet. Newsl. 26:174.

BGS 138, Necrotic leaf spot 4, *nec4*

Stock number: BGS 138
Locus name: Necrotic leaf spot 4
Locus symbol: *nec4*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (1, 2, 3).
Located in chromosome 3H (1, 3).

Description:
Small black spots develop on the leaves (1, 3).

Origin of mutant:
An X-ray induced mutant in Proctor (PI 280420) (1, 3).

Mutational events:
nec4.f (728/63, OUM371) in Proctor (PI 280420) (1, 2, 3, 4).

Mutant used for description and seed stocks:
nec4.f in Proctor (OUM371); *nec4.f* in Bowman (PI 483237)*2 (BW631, NGB 22197).

References:
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Prepared:
J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:175.

BGS 139, Necrotic leaf spot 5, *nec5*

Stock number: BGS 139
Locus name: Necrotic leaf spot 5
Locus symbol: *nec5*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (1, 2, 3).
Located in chromosome 3H (1, 3).

Description:
Circular dark brown spots develop on the leaves (1, 3).

Origin of mutant:
An ethyl methanesulfonate induced mutant in Diamant (PI 330397, PI 467775) (1, 3).

Mutational events:
nec5.g (HLN_{EP}71/48, OUM372) in Diamant (PI 330397, PI 467775) (1, 2, 3, 4).

Mutant used for description and seed stocks:
nec5.g (OUM372) in Diamant; *nec5.g* in Bowman (PI 483237)*2 (BW632, NGB 22109).

References:
1. Fischbeck, G., and H. Häuser. 1976. Research notes. Barley Genet. Newsl. 6:28-29.
2. Fischbeck, G., and H. Häuser. 1978. Cytogenetic studies of some induced barley mutants. Barley Genet. Newsl. 8:36-37.
3. Häuser, J., and G. Fischbeck. 1976. Untersuchungen zur Lokalisierung einiger Mutationen von Gerste (*Hordeum sativum*). Z. Pflanzenzücht. 77:269-280.
4. Søgaaard, B., and P. von Wettstein-Knowles. 1987. Barley: genes and chromosomes. Carlsberg Res. Comm. 52:123-196.

Prepared:
J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:176.

BGS 140, Xantha seedling 8, *xnt8*

Stock number: BGS 140
Locus name: Xantha seedling 8
Locus symbol: *xnt8*

Previous nomenclature and gene symbolization:

Albino seedling b = *alb*, *b* (1).
Xantha seedling h = *xan*, *h* (2).

Inheritance:

Monofactorial recessive (1, 2).
Located in chromosome 3HS (2); about 2.9 cM from the *msg5* (male sterile genetic 5) locus (2).

Description:

Seedlings have a yellow color and die at the two to three leaf stage (1). The *xnt8.h* gene must be maintained as a heterozygous stock. Allelism tests with mutants at the *xnt3* (xantha seedling 3) locus, which is present in the same region of chromosome 3H, have not been conducted.

Origin of mutant:

A spontaneous mutant in Carlsberg II (CIho 10114) (1).

Mutational events:

xnt8.h (GSHO 582) in Carlsberg II (CIho 10114) (1).

Mutant used for description and seed stocks:

xnt8.h (GSHO 582) in Carlsberg II.

References:

1. Rahman, M.M. 1973. Balanced male sterile-lethals systems for hybrid barley production. Ph.D. Thesis, Montana State Univ., Bozeman.
2. Rahman, M.M., and R.F. Eslick. 1976. Linkage of spontaneous mutant seedling lethal genes with genetic male sterile genes. Barley Genet. Newsl. 6:53-58.

Prepared:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:177.

BGS 141, Reaction to barley yellow mosaic virus 5, *rym5*

Stock number: BGS 141
Locus name: Reaction to barley yellow mosaic virus 5 (BaYMV)
Locus symbol: *rym5*

Previous nomenclature and gene symbolization:

Resistance to BaYMV = *Ym* (3, 5, 7).
Resistance to BaYMV 5 = *ym5* (4).
Resistance to BaYMV 5 = *rym5* (8).

Inheritance:

Monofactorial recessive (4).
Located in chromosome 3HL (7); approximately 2.5 cM distal from the *Est1* (esterase 1) locus (4, 7); flanked by molecular markers MWG838 and MWG010A at distances of 0.8 and 1.3 cM, respectively, in 3H bin 16 (1).

Description:

Plants with the *rym5.h* allele are resistant to Japanese strains I and II of BaYMV, but susceptible to Japanese strain III of BaYMV (2). In Germany, plants with *rym5.h* are resistant to strains BaYMV-1 and BaYMV-2 (6, 10). Although plants with *rym5.h* are resistant to BaMMV (barley mild mosaic virus) in Germany (6, 10), they are susceptible to the Japanese strain BaMMV-Na (6, 9).

Origin of mutant:

Natural occurrence in Mokusekko 3 (OUC627, PI 420938) (4).

Mutational events:

rym5.h in Mokusekko 3 (PI 420938) (4).

Mutant used for description and seed stocks:

rym5.h in Misato Golden (OUJ848) from Mokusekko 3 (4).

References:

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5. Konishi, T., and R. Kaiser. 1991. Genetic difference in barley yellow mosaic virus resistance between Mokusekko 3 and Misato Golden. Japan. J. Breed. 41:499-505.
6. Konishi, T. and R. Kaiser-Alexnat. 2000. Reaction of barley accessions to BaYMV and BaMMV in Japan, compared with data in Germany. Barley Genet. Newsl. 30:58-61.
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Prepared:

T. Konishi and J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:90-91.

BGS 142, Brachytic 8, *brh8*

Stock number: BGS 142
Locus name: Brachytic 8
Locus symbol: *brh8*

Previous nomenclature and gene symbolization:

Brachytic-ad = *brh.ad* (4).

Inheritance:

Monofactorial recessive (4, 6, 7).

Located in chromosome 3HL (2, 5); near the *btr1* (non-brittle rachis 1) locus based on linkage drag (5); about 26.3 cM proximal from SSR marker HVM60 in bin 3H-08 (1); *brh8.ad* is associated with SNP markers 2_0931 to 2_0657 (positions 104.39 to 141.21 cM) in 3H bins 07 to 09 of the Bowman backcross-derived line BW100 (2), likely in 3H bin 07.

Description:

In the Bowman backcross-derived line, *brh8* plants are 3/4 to 5/6 of normal height and awns are 2/3 to 3/4 of normal length. The peduncle is 3/4 normal length. The seedling leaf of *brh8* plants is shorter and wider than those of normal sibs and the leaf blades are slightly wider. Kernels of *brh8* plants are shorter than that of normal sibs and their weights are nearly 15% lower. Heading dates are 2 or 3 days later, spikes have 3 to 4 more kernels, and rachis internodes are about 20% shorter. Grain yield is nearly normal (1, 3).

Origin of mutant:

Probably a sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (7).

Mutational events:

brh8.ad (17:16:1, DWS1008, GSHO 1671) in Birgitta (NSGC 1870, NGB 1494) (6, 7).

Mutant used for description and seed stocks:

brh8.ad (GSHO 1671) in Birgitta; *brh8.ad* in Bowman (PI 483237)*8 (GSHO 1944, BW100, NGB 20506).

References:

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5. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
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Prepared:

J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:92.

Revised:

J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:230.

J.D. Franckowiak. 2012. *Barley Genet. Newsl.* 42:232.

BGS 143, Shrunkendosperm xenia 8, *sex8*

Stock number: BGS 143
Locus name: Shrunkendosperm xenia 8
Locus symbol: *sex8*

Previous nomenclature and gene symbolization:

Shrunkendosperm xenia-j = *sex.j* (2).

Inheritance:

Monofactorial recessive (2).

Located in chromosome 3HS (2); based on linkage drag with the *Btr1* (non-brittle rachis 1) locus (2).

Description:

After the hard dough stage, the grain develops a slight depression in the dorsal or lemma side. In plants heterozygous for *sex8*, a xenia pattern of expression is observed. Seeds with a small depression in the dorsal side are homozygous for *sex8*.

Origin of mutant:

A spontaneous mutant in a selection from cross I89-633 (lax-169/3* Bowman) (1).

Mutational events:

sex8.j (GSHO 2471) in I89-633-1 (1, 2); the origin could be from the Bonus (PI 189763) mutant lax.69 (NGB 116402).

Mutant used for description and seed stocks:

sex8.j (GSHO 2471) in I89-633-1; *sex8.j* in Bowman (PI 483237)*7 (GSHO 1945, BW848, NGB 22284).

References:

1. Franckowiak, J.D. (Unpublished).
2. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. Barley Genet. Newsl. 24:63-70.

Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:93.

BGS 144, Slender dwarf 5, *sld5*

Stock number: BGS 144
Locus name: Slender dwarf 5
Locus symbol: *sld5*

Previous nomenclature and gene symbolization:

Indian Dwarf (1, 4).
Slender dwarf-h = *sld.h* (2).

Inheritance:

Monofactorial recessive (1).
Located in chromosome 3HS (2); based on linkage drag with the *Btr1* (non-brittle rachis 1) locus (2).

Description:

Plants with the *sld5.h* gene show reduced vigor and have thin grain. Plants are about 2/3 normal height in the XV 2334-6R line and about 1/2 normal in Indian Dwarf accession (1, 4). Seedlings with the *sld5.h* gene are insensitive to treatment with gibberellic acid (1). The second factor for reduced height in Indian Dwarf may be the *Eam5.x* (early maturity 5, BGS 348) mutant.

Origin of mutant:

A spontaneous mutant identified as Indian Dwarf (CIho 13994) (1).

Mutational events:

sld5.h (DWS1238, GSHO 2483) in XV2334-6R from Indian Dwarf (CIho 13994) (1, 3, 4);
Apam Dwarf likely has an allele at the *sld5* locus (4).

Mutant used for description and seed stocks:

sld5.h (GSHO 2483) in XV2334-6R, *sld5.h* in Bowman (PI 483237)*7 (GSHO 1940, BW865, NGB 22302).

References:

1. Boulger, M.C., R.G. Sears, and W.E. Kronstad. 1982. An investigation of the association between dwarfing sources and gibberellic acid response in barley. p. 550-553. In M.J.C. Asher, R.P. Ellis, A.M. Hayter, and R.N.H. Whitehouse (eds.) Barley Genetics IV. Proc. Fourth Int. Barley Genet. Symp., Edinburgh. Edinburgh Univ. Press, Edinburgh.
2. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. Barley Genet. Newsl. 24:63-70.
3. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. Barley Genet. Newsl. 21:116-127.
4. Sears, R.G., W.E. Kronstad, and R.J. Metzger. 1981. Inheritance of dwarf and semidwarf plant height in barley. Crop Sci. 21:828-831.

Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:94.

BGS 146, Calcaroides-d, *cal-d*

Stock number: BGS 146
Locus name: Calcaroides-d
Locus symbol: *cal-d*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (5, 6).
Located in chromosome 3H (7); near the centromere and near molecular marker CDO684 (7); associated with SNP markers 1_0672 to 2_1502 (positions 58.56 to 100.48 cM) in 3H of the Bowman backcrossed-derived line BW106 (2), in 3H bin 06.

Description:
At the tip of the lemma proper, in a position corresponding to the transition between lemma and awn, *cal-d* mutants bear a well-organized ectopic structure, the sac (1, 54). Only the allele *cal-d.22* does not produce pronounced lemma wings. The *cal-d* mutants bear a short distal awn (7). In contrast to the *Kap1* (hooded lemma 1) phenotype, the sac does not develop into an epiphyllous flower. The *cal-d* alleles are associated with leaf curling also (7). The awn malformation of *cal-d* mutants is associated with developmental activation of the phytomeric triad separating the lemma from awn (4). Plants of the Bowman backcross-derived line for *cal-d.4*, BW106, were about 3/4 of normal height and headed one day later than Bowman. Awns were 1/2 and peduncles were 2/3 of normal length and leaf blades were slightly narrower. Kernels of BW106 were thin and weighted about 1/3 less than those of Bowman. Test weights were low and grain yields were less than 1/2 of normal (3).

Origin of mutant:
An X-ray induced mutant in Foma (CIho 11333) (6, 7).

Mutational events:
cal-d.4 (GSHO 1698, NGB 114284) in Foma (CIho 11333) (6); *cal-d.14* (NGB 119381) in Kristina (NGB 1500), *-d.18* (NGB 114297), *-d.22* (NGB 114301, 114302) in Bonus (PI 189763) (6).

Mutant used for description and seed stocks:
cal-d.4 (NGB 114284, GSHO 1698) in Foma; *cal-d.4* in Bowman (PI 483237)*6 (GSHO 1875); *cal-d.4* in Bowman*7 (BW106, NGB 20512).

References:
1. Bossinger, G., U. Lundqvist, W. Rohde, and F. Salamini. 1992. Genetics of plant development in barley. p. 989-1017. *In* L. Munck, K. Kirkegaard, and B. Jensen (eds.). Barley Genetics VI. Proc. Sixth Int. Barley Genet. Symp., Helsingborg, 1991. Munksgaard Int. Publ., Copenhagen.
2. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. Plant Physiology. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
3. Franckowiak, J.D. (Unpublished).
4. Franckowiak, J.D., B.P. Forster, U. Lundqvist, J. Lyon, I. Pitkethly, and W.T.B. Thomas. 2010. Developmental mutants as a guide to the barley phytomer. pp. 46-60. *In*: S. Ceccarelli and S. Grandi (eds), Proc. 10th International Barley Genetics Symposium, 5-10 April 2008, Alexandria Egypt. ICARDA, PO Box 5466, Aleppo, Syria.
5. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. Hereditas 62:409-414.

6. Lundqvist, U. 1993 Coordinator's report: Ear morphology genes. Barley Genet. Newsl. 22:137-139.

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Prepared:

U. Lundqvist and J. D. Franckowiak. 2002. Barley Genet. Newsl. 32:97.

Revised:

U. Lundqvist and J. D. Franckowiak. 2010. Barley Genet. Newsl. 40:58-59.

BGS 147, Multiovary 2, *mov2*

Stock number: BGS 147
Locus name: Multiovary 2
Locus symbol: *mov2*

Previous nomenclature and gene symbolization:

Multi-ovary = *mo* (4).
Multiovary 7 = *mo7a* (5, 6).

Inheritance:

Monofactorial recessive (2, 4, 5, 6).
Located in chromosome 3HS (6); co-segregation with molecular markers ABC171A and JS001B in 3H bin 02 (6).

Description:

The *mov2.g (mov7a)* mutant has between five and seven carpel-like structures and normal lodicules. Stamens are not present, but some carpels are terminated with stamen-like structures. Pollination using wild-type flowers results in a few seeds (6). The plant appears abnormal with a twisted and compact spike and reduced awn length. The frequency of mutant plants in the two F₂ progenies examined was much lower than expected (6). The stock must be maintained as a heterozygote (3). The mutants reported by Moh and Nilan (4) and Kamra and Nilan (2) may be alleles, but seed stocks were unavailable for testing (6).

Origin of mutant:

A fast neutron induced mutant in Steptoe (Clho 15229) (5).

Mutational events:

mov2.g (mo7a) in Steptoe (Clho 15229) (5, 6); *mov2.a (mo1)* (4, 6); *mov2.c (mo3)* (1, 2, 6).

Mutant used for description and seed stocks:

mov2.g (mo7a) in Steptoe.

References:

1. Kamra, P. 1966. Genetic control of the development of floral organs in *Hordeum vulgare*. p. 213-215. In A. Lengerova (ed.) Mechanisms of Mutation and Inducing Factors. Academia, Prague.
2. Kamra, O.P., and R.A. Nilan 1959. Multi-ovary in barley. Floral anatomy and embryo-sac development. J. Hered. 50:159-165.
3. Kleinhofs, A. (Unpublished).
4. Moh, C.C., and R.A. Nilan. 1953. Multi-ovary in barley. A. mutant induced by atomic radiation. J. Hered. 44:183-184.
5. Soule, J., I. Skodova, D. Kudrna, A. Kilian, and A. Kleinhofs. 1995. Molecular and genetic characterization of barley flower development mutants. Barley Genet. News! 25:76-80.
6. Soule, J.D., D.A. Kudrna, and A. Kleinhofs. 2000. Isolation, mapping, and characterization of two barley multiovary mutants. J. Hered. 91:483-487.

Prepared:

A. Kleinhofs. 2005. Barley Genet. News! 35:190.

BGS 148, Brachytic 14, *brh14*

Stock number: BGS 148
Locus name: Brachytic 14
Locus symbol: *brh14*

Previous nomenclature and gene symbolization:

Brachytic-q = *brh.q* (4).

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 3HL (2); approximately 24.9 cM proximal from SSR marker Bmac0029 in 3H bin 15 (2).

Description:

Plants are about 2/3 normal height, and awns are 1/3 to 3/4 normal, peduncles are about 2/3 normal length, and rachis internodes are about 7/8 normal length (2, 6, 7). Seedling leaves of *brh14.q* plants are relatively short, but they do respond to gibberellic acid treatment (1). Leaf blades are about 3/4 normal length. The kernels of *brh14* plants are slightly shorter and smaller than those of normal sibs, but there are slightly more kernels per spike. However, the grain yields of the *brh14* line to average 1/3 to 1/4 of those for Bowman reduced because tillering was reduced. Plants show an erect growth habit (2, 3). Failure of the internode below the peduncle to elongate was observed in double dwarfs involving *brh14.q* in the Akashinriki genetic background (7).

Origin of mutant:

An ethyl methanesulfonate induced mutant in Akashinriki (OUJ659, PI 467400) (6, 7).

Mutational events:

brh14.q (OUM131, dw-d, DWS1035, GSHO 1682) in Akashinriki (OUJ659, PI 467400) (4, 5, 6, 7).

Mutant used for description and seed stocks:

brh14.q (GSHO 1682) in Akashinriki; *brh14.q* in Bowman (PI 483237)*6 (GSHO 2175, BW085, NGB 20492).

References:

1. Börner, A. 1996. GA response in semidwarf barley. *Barley Genet. Newsl.* 25:24-26.
2. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. *J. Hered.* 96:654-662.
3. Franckowiak, J.D. (Unpublished).
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7. Konishi, T. 1977. Effects of induced dwarf genes on agronomic characters in barley. p. 21-38. *In* Use of dwarf mutations. Gamma-Field Symposium No. 16.

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:231.

BGS 149, Reaction to *Puccinia coronata* var. *hordei* 1, *Rpc1*

Stock number: BGS 149
Locus name: Reaction to *Puccinia coronata* var. *hordei* 1
Locus symbol: *Rpc1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial dominant (3).

Located in chromosome 3H centromeric region (1); approximately 2.5 cM from RAPD marker OPO08-700 (1).

Description:

Crown rust of barley was identified as a new disease of barley in North America (2). In seedling tests, resistant cultivars exhibited necrotic or chlorotic flecks (0; to ; infection types) at infection sites and no sporulation (3). Adult plant reactions of Hor2596 were resistant to moderately resistant (3). Hor 2596 is one of the differential lines for barley leaf rust (caused by *Puccinia hordei*), see BGS 032, *Rph9.i* (reaction to *Puccinia hordei* 9). The F1 plants from the Bowman/Hor2596 cross exhibited slightly higher infection types (1,2 reaction) than the resistant parent (3).

Origin of mutant:

Natural occurrence in Abyssinian (Hor 2596, Clho 1234) (3).

Mutational events:

Rpc1.a in Hor 2596 (GSHO 1601) (3).

Mutant used for description and seed stocks:

Rpc1.a in Hor 2596 (GSHO 1601) (3).

References:

1. Agrama, H.A., L. Dahleen, M. Wentz, Y. Jin, and B. Steffenson. 2004. Molecular mapping of the crown rust resistance gene *Rpc1* in barley. *Phytopathology* 94:858-861.
2. Jin, Y., and B. Steffenson. 1999. *Puccinia coronata* var. *hordei* nov.: morphology and pathogenicity. *Mycologia* 91:877-884.
3. Jin, Y., and B. Steffenson. 2002. Sources and genetics of crown rust resistance in barley. *Phytopathology* 92:1064-1067.

Prepared:

Y. Jin and J.D. Franckowiak. 2007. *Barley Genet. Newsl.* 37:232.

BGS 150, Scirpoides leaf-b, *scl-b*

Stock number: BGS 150
Locus name: Scirpoides leaf-b
Locus symbol: *scl-b*

Previous nomenclature and gene symbolization:

Scirpoides leaf-5 = *scl.5* (3).

Inheritance:

Monofactorial recessive (2).

Probably located on chromosomes 3HL or 6HS (1); associated with SNP markers 2_0130 to 1_1172 (positions 151.97 to 190.87 cM) in 3HL and with SNP markers 1_0061 to 1_1205 (positions 70.15 to 82.43 cM) in 6HS of the Bowman backcross-derived line BW777 (1).

Description:

Leaf blades of *scl-b* plants are folded inward and are narrow compared to those of normal sibs. Folding of the leaf blade persists until maturity (2, 3). Plants of Bowman backcross-derived line BW777 were 15% shorter than Bowman, kernels were narrower and 15% lighter, and grain yields were about 25% lower (2). Plants of BW777 have inward folded leaf blades that are less than 2/3 as wide as those of Bowman (2). When grown in the greenhouse *scl-b.5* plants had very narrow leaf blades that showed more inward folding than *scl-a* mutants. Also, the awns of spikes were often trapped by the collar of the flag leaf during spike emergence (2). A new locus symbol is recommended based on the morphological differences compared to *scl-a* mutants and the lack of SNP markers retained in chromosome 1HL (1, 2).

Origin of mutant:

A mutant was induced by UV-ray treatment of pollen grains of Bonus (PI 189763) (3).

Mutational events:

scl-b.5 (NGB 117103) in Bonus (PI 189763) (3).

Mutant used for description and seed stocks:

scl-b.5 (NGB 117103) in Bonus; *scl-b.5* in Bowman (PI 483237)*3 (BW777, NGB 20754).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. Plant Physiology. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Franckowiak, J.D. (Unpublished).
3. Lundqvist, U. (Unpublished).

Prepared:

U. Lundqvist and J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:60.

BGS 151, Chlorina seedling 9, *fch9*

Stock number: BGS 151
Locus name: Chlorina seedling 9
Locus symbol: *fch9*

Previous nomenclature and gene symbolization:

Chlorina k = f_k (2).
Chlorina 9 = *f9* (1, 3).

Inheritance:

Monofactorial recessive (2).
Located in chromosome 4HS (2); over 22.7 cM distal from the *Kap1* (hooded lemma 1) locus (2).

Description:

Seedling leaves are yellow green in color, and the yellow green color persists until near maturity (2). Plants grown in the field are stunted and maturity is delayed.

Origin of mutant:

An X-ray induced mutant in Ko A (OUJ215, PI 383935) (2).

Mutational events:

fch9.k (Kmut 174, OUM288, GSHO 571) in Ko A (OUJ215, PI 383935) (2).

Mutant used for description and seed stocks:

fch9.k (GSHO 571) in Ko A; *fch9.k* in Bowman (PI 483237)*7 (GSHO 1996); *fch9.k* in Bowman*9 (BW365, NGB 20604).

References:

1. Robertson, D.W. 1971. Recent information of linkage and chromosome mapping. p. 220-242. In R.A. Nilan (ed.) Barley Genetics II. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
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Prepared:

T.E. Haus and T. Tsuchiya. 1971. Barley Genet. Newsl. 1:137.

Revised:

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:178.

BGS 152, Hooded lemma 1, *Kap1*

Stock number: BGS 152
Locus name: Hooded lemma 1
Locus symbol: *Kap1*

Previous nomenclature and gene symbolization:

Hooded lemma = *K* (9).
Hooded lemma = *A* (10).
Hooded = *C*₁ (3).

Inheritance:

Monofactorial dominant (1, 3, 8).
Located in chromosome 4HS (1); about 25.1 cM proximal from the *glf3* (glossy leaf 3) locus (6).

Description:

The hooded ("Kapuze") trait is characterized by an appendage to the lemma, which develops as a trifurcate structure consisting of a deformed floret at its center with two triangular leaf-like projections called lemma wings. The supernumerary floret often contains stamens with fertile pollen grains and occasionally bears a kernel within it (5, 6, 11). The ectopic expression of the *Kap1.a* allele forms the extra floret and is associated with the presence of a 305-base pair duplication in intron 4 of the *Knox3* sequence (4).

Origin of mutant:

Natural occurrence in many cultivars (5, 7); probably one spontaneous event early during the domestication of barley (4).

Mutational events:

Kap1.a in an unknown cultivar (4, 7); *Kap1.e* (*K*^e, elevated hooded) a mutant of the *Kap1.a* allele in an unknown cultivar (BGS 153, GSHO 763, Chengchou 5) (4, 7).

Mutant used for description and seed stocks:

Kap1.a in Colseas (GSHO 985); *Kap1.a* from Strip Tease (CIho 6837) in Betzes (PI 129430)*7 (PI 533600, Haybet), *Kap1.a* from CIho 2220 in Compana (PI 537442)*7 (PI 534506) (2); *Kap1.a* from R.I. Wolfe's Multiple Dominant Marker Stock in Bowman (PI 483237)*8 (GSHO 2007, BW431, NGB 20663).

References:

1. Buckley, G.F.H. 1930. Inheritance in barley with special reference to the color of caryopsis and lemma. *Sci. Agric.* 10:460-492.
2. Hockett, E.A., and H.F. Bowman. 1990. Registration of hooded barley isogenic lines. *Crop Sci.* 30:754-755.
3. Miyake, K., and Y. Imai. 1922. [Genetic studies in barley. 1.] *Bot. Mag., Tokyo* 36:25-38. [In Japanese.]
4. Müller, K.J., N. Romano, O. Gerstner, F. Gracia-Maroto, C. Pozzi, F. Salamini, and W. Rohde. 1995. The barley *Hooded* mutation caused by a duplication in a homeobox gene intron. *Nature* 374:727-730.
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Prepared:

T.E. Haus and T. Tsuchiya. 1971. Barley Genet. Newsl. 1:138.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:179-180.

BGS 155, Glossy leaf 1, *glf1*

Stock number: BGS 155
Locus name: Glossy leaf 1
Locus symbol: *glf1*

Previous nomenclature and gene symbolization:

Waxless bloom on leaves = *w1* (13).

Glossy = *gl* (11).

Glossy leaves = *gl* (18).

Glossy leaf = *gl* (17).

Glossy seedling 2 = *gl2* (5, 11).

Eceriferum-zh = *cer-zh* (6).

Inheritance:

Monofactorial recessive (11).

Located in chromosome 4HL (5, 11, 14, 16); about 7.5 cM distal from the *lbi2* (long basal rachis internode 2) locus (2); about 4.8 cM distal from the *Mlg* (*Reg2*, reaction to *Erysiphe graminis* 2) locus (2); associated with SNP markers 2_0820 to 1_0606 (positions 89.78 to 95.92 cM) in 4HL of the Bowman backcross-derived line BW385 (1), in 4H bin 06.

Description:

Surface wax coating on the leaf blade appears absent from the seedling stage to near maturity, and leaves have a shiny appearance (wax code ++ ++ -) (6). Plants are semidwarf, relatively weak, and late in heading. The stock in the Bonus is highly sterile (6), but the Bowman backcross-derived line has nearly complete fertility. The lack of surface waxes reduces the ability of growing germ tube of certain fungi to find the stomata openings (12). Plants of Bowman backcross-derived line BW385 were 5 to 15% shorter than Bowman and headed about 2 days later. Kernel weights were about 20% lower and grain yields were approximately 3/4 of normal (3).

Origin of mutant:

A radiation induced mutant in Himalaya (CIho 1312) (11, 15), an X-ray induced mutant in Bonus (PI 189763) (6).

Mutational events:

glf1.a (GSHO 98), *glf1.b* (*gl2*, GSHO 22) in Himalaya (CIho 1312) (15); *glf1.f* in 34-119-1, *glf1.g* in II-34-199-7-2 (GSHO 89) (4); *cer-zh.54* (NGB 110938, GSHO 455) in Bonus (6, 7); *cer-zh.266* (NGB 111153), *-zh.308* (NGB 111195), *-zh.357* (NGB 111244, NGB 117254), *-zh.366* (NGB 111253), *-zh.432* (NGB 111320), *-zh.433* (NGB 111321, NGB 117256) in Foma (CIho 11333) (7, 10); *cer-zh.325* (NGB 111212) in Foma (7); *cer-zh.373* (NGB 111260) in Foma (8); *cer-zh.865* (NGB 111753) in Bonus (9); *glf1.h* (MXM137) in Morex (CIho 15773) based on phenotype and SNP markers retained in the Bowman backcross-derived line BW384 (1, 3).

Mutant used for description and seed stocks:

glf1.a (GSHO 98) in Himalaya; *cer-zh.54* (GSHO 455, NGB 110938) in Bonus was used for allelism tests; *glf1.a* via R.I. Wolfe's chromosome 4 multiple recessive marker stock in Bowman (PI 483237)*8 (GSHO 2015, BW385, NGB 20623); *cer-zh.54* in Bowman*3 (BW164, NGB 21996); *glf1.h* in Bowman*5 (BW384, NGB 22146).

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1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. Plant Physiology. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.

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3. Franckowiak, J.D. (Unpublished).
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Prepared:

- T.E. Haus and T. Tsuchiya. 1971. Barley Genet. Newsl. 1:141 as BGS 155, Glossy seedling, *gl*; and Barley Genet. Newsl. 1:145 as BGS 159, Glossy seedling 2, *gl*2.
U. Lundqvist. 1975. Barley Genet. Newsl. 5:144 as BGS 426, Eceriferum-zh, *cer-zh*.

Revised:

- T. Tsuchiya. 1980. Barley Genet. Newsl. 10:114 as BGS 155, Glossy seedling, *gl*; and Barley Genet. Newsl. 10:116 as BGS 159, Glossy seedling 2, *gl*2.
U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:181-182.
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BGS 156, Long basal rachis internode 2, *lbi2*

Stock number: BGS 156
Locus name: Long basal rachis internode 2
Locus symbol: *lbi2*

Previous nomenclature and gene symbolization:

Long basal rachis internode 2 = *lb2* (3).
Erectoides-i = *ert-i* (4, 5, 6).

Inheritance:

Monofactorial recessive (2, 3).
Located in chromosome 4HL (3, 6); less than 12.8 cM proximal from the *Kap1* (hooded lemma 1) locus (3, 5); about 2.4 cM proximal from the *Kap1* locus (4); about 18.5 cM proximal from the *glf1* (glossy leaf 1) locus (7).

Description:

Mutant plants in the cultivar Montcalm have a marked elongation and weakness of the basal rachis internode of the spike. This region may be 10 to 13 cm long in some tillers. The spike hangs vertically downward from the collar on emergence from the sheath and is often broken off in this region by the wind. Even when not broken off, spikes have a high degree of sterility and contain poorly filled grain. Plants show delayed maturity (3). The *ert-i* mutants in Bonus have an erect, semicompact (rachis internode length ranging from 2.3 to 2.9 mm) spike, an elongated (2 to 4 cm) basal rachis internode, and reduced plant height (3/4 normal) (6). Removal of modifiers from the Montcalm and Bonus mutant stocks by backcrossing produces Bowman backcross-derived lines having similar phenotypes (1).

Origin of mutant:

A gamma-ray induced mutant in Montcalm (CIho 7149) (3).

Mutational events:

lbi2.b (Alb Acc 1028, GSHO 572) in Montcalm (CIho 7149) (3); *ert-i.27* (NGB 112627, GSHO 482), *-i.53* (NGB 112652) in Bonus (PI 189763) (1, 2); *ert-i.126* (NGB 112725) in Bonus (6).

Mutant used for description and seed stocks:

lbi2.b (GSHO 572) in Montcalm; *ert-i.27* (NGB 112627, GSHO 482) in Bonus; *lbi2.b* in Bowman (PI 483237)*7 (GSHO 2009, BW472, NGB 20702); *ert-i.27* in Bowman*7 (GSHO 2008, BW311, NGB 22107).

References:

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2. Hagberg, A., Å. Gustafsson, and L. Ehrenberg. 1958. Sparsely contra densely ionizing radiations and the origin of erectoid mutants in barley. Hereditas 44:523-530.
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Prepared:

- T.E. Haus and T. Tsuchiya. 1971. Barley Genet. Newsl. 1:142.
Revised:
J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:183.

BGS 157, Brachytic 2, *brh2*

Stock number: BGS 157
Locus name: Brachytic 2
Locus symbol: *brh2*

Previous nomenclature and gene symbolization:

Brachytic 2 = *br2* (9).
Breviaristatum-I = *ari-I* (4, 5).

Inheritance:

Monofactorial recessive (8).
Located in chromosome 4HL (8); about 1.5 cM proximal from the *glf3* (glossy leaf 3) locus (3, 8); over 22.8 cM proximal from the *Kap1* (hooded lemma 1) locus (8); near AFLP marker E4140-7 in subgroup 38-40 of the Proctor/Nudinka map (7); about 15.9 cM distal from SSR marker Bmag0353 near the boundary between 4H bins 06 and 07 (2).

Description:

Plant height and vigor are reduced to about 2/3 normal; the awn is less than 1/4 normal length; the spike is semi-compact; and the leaf, kernel, glume and glume awn, rachilla, and coleoptile are shorter than in the original cultivar. Auricles are well developed and larger than those of the original cultivar (9). In the Bowman backcross-derived lines, the peduncle is about 1/2 normal length, kernel weights are slightly over 2/3 normal, yield is about 1/2 normal; however, rachis internode lengths are normal (2). The *ari-I.3* allele at the *brh2* locus is sensitive to gibberellic acid treatment (1).

Origin of mutant:

An X-ray induced mutant in Svanhals (PI 5474) (9).

Mutational events:

brh2.b (Kmut 28, OUM283, GSHO 573) in Svanhals (PI 5474) (8); *ari-I.3* (NGB 115848) in Bonus (PI 189763) (5); *ari-I.132* (NGB 115942) in Foma (CIho 11333) (6); *ari-I.135* (NGB 115945), *-I.145* (NGB 115956), *-I.214* (NGB 116023), *-I.237* (NGB 116047) in Foma, *-I.257* (NGB 116066) in Kristina (NGB 1500) (5).

Mutant used for description and seed stocks:

brh2.b (GSHO 573) in Svanhals; *ari-I.3* (GSHO 1660) in Bonus; *brh2.b* in Bowman (PI 483237)*7 (GSHO 2016, BW090, NGB 20496); *ari-I.3* in Bowman*7 (GSHO 2017, BW050, NGB 20458).

References:

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2. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. J. Hered. 96:654-662.
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9. Tsuchiya, T. 1962. Radiation breeding in two-rowed barley. Seiken Zihō 14:21-34.

Prepared:

T.E. Haus and T. Tsuchiya. 1971. Barley Genet. Newsl. 1:143.

Revised:

T. Tsuchiya. 1980. BGN 10:115.

J.D. Franckowiak and U. Lundqvist. 1997. Barley Genet. Newsl. 26:184.

J.D. Franckowiak and L.S. Dahleen. 2007. Barley Genet. Newsl. 37:235-236.

BGS 158, Yellow head 1, *yhd1*

Stock number: BGS 158
Locus name: Yellow head 1
Locus symbol: *yhd1*

Previous nomenclature and gene symbolization:

Yellow head = *yh* (5).

Inheritance:

Monofactorial recessive (4, 5).

Located in chromosome 4HL (4); over 8.7 cM distal from the *Hsh1* (hairy leaf sheath 1) locus (3, 4); *yhd1.a* is associated with SNP markers 1_0712 to 2_0013 (positions 170.17 to 183.54 cM) in 4H bins 12 to 13 of the Bowman backcross-derived line BW920 (1).

Description:

The immature spikes appear ivory to pale yellow in color; the lemma is ivory-colored, but terminates into green tip with green awns; the plant has a whitish lower leaf sheath and ivory-colored culm nodes and rachis internodes (4). The pattern of reduced chlorophyll development is similar to the *alm1* (albino lemma 1) mutants. Plants of Bowman-backcross-derived line for *yhd1.a*, BW920, headed and matured slightly earlier than Bowman and kernels were slightly lighter (2).

Origin of mutant:

A spontaneous mutant in an unknown cultivar (4).

Mutational events:

yhd1.a (OUL012, GSHO 574) in Kimugi (4).

Mutant used for description and seed stocks:

yhd1.a (GSHO 574) in Kimugi; *yhd1.a* in Bowman (PI 483237)*8 (GSHO 2028, BW920, NGB 22349).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
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4. Takahashi, R., and J. Hayashi. 1966. Inheritance and linkage studies in barley. II. Assignment of several new mutant genes to their respective linkage groups by the trisomic method of analysis. *Ber. Ohara Inst. landw. Biol., Okayama Univ.* 13:185-198.
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Prepared:

T.E. Haus and T. Tsuchiya. 1971. *Barley Genet. Newsl.* 1:144.

Revised:

J. D. Franckowiak and T. Konishi. 1997. *Barley Genet. Newsl.* 26:185.
J.D. Franckowiak. 2012. *Barley Genet. Newsl.* 42:250.

BGS 160, Enhancer of minute, *en-min*

Stock number: BGS 160
Locus name: Enhancer of minute
Locus symbol: *en-min*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive, but expressed only in plants homozygous for the *min1.a* (semi-minute dwarf 1) allele (3).
Location is unknown.

Description:
Plants are extremely dwarfed with the adult plant being less than 5 cm tall. The leaf blade and sheath are very short and thick and have a whitish dark green color. Roots are thick and short with C-tumor-like swelling at their tips. No spikes are formed; hence, the stock must be maintained as a heterozygote at the *min1* locus (2). Among the kernels produced by heterozygous plants, those that will give rise to minute plants have a markedly shrunken endosperm (1, 2). Tissues of the plant are mixoploid with 2x, 3x, 4x, and up to 60x cells being formed by abnormal cytokinesis (1, 2).

Origin of mutant:
A spontaneous mutant at the *min1* locus in Kaiyo Bozu (OUJ378, PI 467405) permits expression of *en-min* (2).

Mutational events:
Natural occurrence of *en-min* (OUL921, GSHO 266) in Kaiyo Bozu (OUJ378, PI 467405) (2).

Mutant used for description and seed stocks:
en-min in a line of Kaiyo Bozu (GSHO 266) that is heterozygous at the *min1* locus.

References:
1. Morikawa, T., and E. Gomi. 1996. Pleiotropism of minute gene (*min*) of barley. p. 530-532. In A.E. Slinkard, G.J. Scoles, and B.G. Rosnagel (eds.) Proc. Fifth Int. Oat Conf. & Seventh Int. Barley Genet. Symp., Saskatoon. Univ. of Saskatchewan, Saskatoon.
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3. Takahashi, R., A. Mochizuki, and J. Hayashi. 1959. Heritable mixoploidy in barley. II. On the semi-minute. Nogaku Kenkyu 47:95-104. [In Japanese with English summary.]

Prepared:
R. Takahashi. 1972. Barley Genet. Newsl. 2:185.

Revised:
T. Konishi and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:186.

BGS 161, Semi-minute dwarf 1, *min1*

Stock number: BGS 161
Locus name: Semi-minute dwarf 1
Locus symbol: *min1*

Previous nomenclature and gene symbolization:

Dwarf = *d* (2).
Semi-minute = *min* (3).

Inheritance:

Monofactorial recessive (2), but interaction with the recessive allele at the *en-min* (enhancer of minute) locus is observed in some cultivars (3).
Located in chromosome 4HL (3, 4); about 6.7 cM distal from the *glf3* (glossy leaf 3) locus (1, 4).

Description:

Plants are 1/2 as tall as the original cultivar, spikes and awns are slightly shorter, and the number of tillers, spikelets per spike, and numbers of kernels are slightly less than in the original cultivar (2). In meristematic tissues of root tips and young shoots, polyploid nuclei consisting of 4x, 8x, and sometimes many more chromosomes are found together with normal diploid cells. Epidermal cells of the leaves are sometimes irregular and variable in shape and size. The mixoploid condition of tissues is believed to result from incomplete cytokinesis following nuclear division (4). Plant vigor in the Bowman backcross-derived line is very sensitive to environmental stress. When grown in the greenhouse, the plants are 2/3 normal height, spike size and length are reduced, and leaves are narrow. Under field conditions, plants are diminutive (less than 1/4 normal height and size) and seed set is low.

Origin of mutant:

A spontaneous mutant in Taishomugi (OUJ 026) (2).

Mutational events:

min1.a (OUJ026, GSHO 987) in Taishomugi (OUJ 026) with the *En-min* gene in the genetic background (2, 4).

Mutant used for description and seed stocks:

min1.a (GSHO 987) in Taisho-mugi; *min1.a* in Bowman (PI 483237)*7 (GSHO 2023. BW515, NGB 20743).

References:

1. Forster, B.P. 1993. Coordinator's report: Chromosome 4. Barley Genet. Newsl. 22:75-77.
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3. Takahashi, R., A. Mochizuki, and J. Hayashi. 1959. Heritable mixoploidy in barley. II. On the semi-minute. Nogaku Kenkyu 47:95-104. [In Japanese with English summary.]
4. Takahashi, R., T. Tsuchiya, and I. Moriya. 1964. [Heritable mixoploidy in barley. III.] Nogaku Kenkyu 50:123-132. [In Japanese.]

Prepared:

R. Takahashi. 1972. Barley Genet. Newsl. 2:186.

Revised:

T. Konishi and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:187.

BGS 163, Spring growth habit 1, *sgh1*

Stock number: BGS 163
Locus name: Spring growth habit 1
Locus symbol: *sgh1*

Previous nomenclature and gene symbolization:

Light sensitiveness = *ls* (2).
Spring habit of growth 1 = *sh1* (3).

Inheritance:

Monofactorial recessive (2).
Located in chromosome 4HL (2); about 5.1 cM distal from the *Hsh1* (hairy leaf sheath 1) locus (1, 4).

Description:

The *sgh1.a* allele conditions a highly spring habit (grade I) and plants readily form ear primordia under long-day conditions without prior cold treatment. However, the type cultivar, Iwate Mensury C, and some other cultivars, which are homozygous for the *sgh1.a* allele, behave as a winter type when sown in the fall (short-day condition) (2, 3, 6). When near-isogenic lines for growth habit are grown at Kurashiki, Japan, the *sgh1.a* allele has little influence on maturity or phenotype in the presence of the other spring habit of growth genes (7). Cultivars having only the *sgh1.a* allele for spring habit are rare (5, 6). The *sgh1.a* allele is found rarely in spring barley cultivars from Tibet (8).

Origin of mutant:

Natural occurrence in many cultivars (3, 5).

Mutational events:

sgh1.a in many cultivars in the so-called Occidental region, and in most cases *sgh1.a* is accompanied by the dominant allele at the *Sgh2* (spring growth habit 2) locus (5).

Mutant used for description and seed stocks:

sgh1.a in Iwate Mensury C (OUJ308, GSHO 575); *sgh1.a* in Hayakiso 2 (OUJ064)*11 (7); *sgh1.a* in Dairokkaku 1 (OUJ654)*11 (7).

References:

1. Takahashi, R., J. Hayashi, and S. Yasuda. 1957. [Four genes in linkage in barley, which are inherited independently of the markers in the known seven linkage groups in barley.] *Nogaku Kenkyu* 45:1-10. [In Japanese.]
2. Takahashi, R., and J. Yamamoto. 1951. [Physiology and genetics of ear emergence in barley and wheat. I. The inheritance and linkage of "light sensitiveness" in barley.] *Nogaku Kenkyu* 40:13-24. [In Japanese.]
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6. Yasuda, S. 1969. [Physiology and genetics of ear emergence in barley and wheat. VIII. Effects of four genes for spring habit on earliness in barley.] *Nogaku Kenkyu* 53:99-113. [In Japanese.]
7. Yasuda, S. 1981. Comparison of yield and some yield components among strains with different genetic combinations of spring genes in barley. *Barley Genet. Newsl.* 11:38-40.

8. Yasuda, S., J. Hayashi, and I. Moriya. 1986. Genotype differentiation in spring growth habit of barley strains collected from northern parts of Pakistan and India. Barley Genet. Newsl. 16:18-19.

Prepared:

S. Yasuda. 1972. Barley Genet. Newsl. 2:188.

Revised:

T. Konishi and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:188.

BGS 164, Hairs on lemma nerves 1, *Hln1*

Stock number: BGS 164
Locus name: Hairs on lemma nerves 1
Locus symbol: *Hln1*

Previous nomenclature and gene symbolization:

Hairs on lemma nerves = *Hn* (3).

Inheritance:

Monofactorial dominant when crossed to a cultivar having abundant barbs on the lemma nerves (2, 3).

Located in chromosome 4HL (2); over 8.7 cM proximal from the *ych1* (yellow head 1) locus; over 22.5 cM distal from the *mlo* (reaction to *Erysiphe graminis hordei-o*) locus (1, 2); complete linkage with the dominant allele at the *Hsh1* (hairy leaf sheath 1) locus has been observed (3).

Description:

A few hairs of 1 to 2 mm are mixed with the ordinary teeth or barbs on the lateral nerves of the lemma (2, 3). Expression of the *Hln1.a* gene may be easier to observe as 1 mm hairs on the tip of sterile lateral kernels in two-rowed barley. The *Hln1* gene is associated with a recessive short awn trait (2/3 of normal length).

Origin of mutant:

Natural occurrence in a number of cultivars from Japan and Korea (3).

Mutational events:

Hln1.a in Kogane-mugi (OUL010) and in several other cultivars (3).

Mutant used for description and seed stocks:

Hln1.a in Kogane-mugi (PI 225020, GSHO 576); *Hln1.a* from Clho 6884 in Bowman (PI 483237)*4 (GSHO 2027). (BW 415, NGB 20648).

References:

1. Hayashi, J., and R. Takahashi. 1986. Location of *hs* for hairy sheath and *yh* for yellow head character on barley chromosome 4. Barley Genet. Newsl. 16:24-27.
2. Takahashi, R., and J. Hayashi. 1966. Inheritance and linkage studies in barley. II. Assignment of several new mutant genes to their respective linkage groups by the trisomic method of analysis. Ber. Ohara Inst. landw. Biol., Okayama Univ. 13:185-198.
3. Takahashi, R., J. Hayashi, and S. Yasuda. 1957. [Four genes in linkage in barley, which are inherited independently of the markers in the known seven linkage groups in barley.] Nogaku Kenkyu 45:1-10. [In Japanese.]

Prepared:

R. Takahashi. 1972. Barley Genet. Newsl. 2:189.

Revised:

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:189.

BGS 165, Glossy leaf 3, *glf3*

Stock number: BGS 165
Locus name: Glossy leaf 3
Locus symbol: *glf3*

Previous nomenclature and gene symbolization:

Glossy leaf = *gl* (3).
Glossy leaf 3 = *gl3* (15).
Glossy leaves 4 = *gl4* (3, 18, 19, 20).
Eceriferum-j = *cer-j* (3, 6).

Inheritance:

Monofactorial recessive (15, 17).
Located in chromosome 4HL (1, 5, 15); about 1.5 cM distal from the *brh2* (brachytic 2) locus (4); over 13.7 cM from the *sid1* (single elongated internode 1) locus (4).

Description:

Surface wax coating on the leaf blades appears absent from the seedling stage to near maturity, and leaves have a shiny appearance (wax code ++ ++ -) (6). Concerning the chemical epicuticular wax composition, the *cer-j* mutant in Bonus produces 34% less wax compared to the wild type, the primary alcohols are the largest wax class. The wax occurs as many very thin plates and as few large irregularly shaped bodies (2, 14, 21).

Origin of mutant:

A spontaneous mutant in Goseshikoku (OUJ128) (15).

Mutational events:

glf3.c (Goseshikoku-hen, OUL032, GSHO 577) in Goseshikoku (OUJ128) (16); *glf3.d* (*gl4*, GSHO 1376) in Gateway (CIho 10072) (20); *cer-j.59* (NGB 110943, GSHO 431), - *j.62* (NGB 110946) in Bonus (PI 189763) (6, 7); *cer-j.71* (NGB 110955), - *j.142* (NGB 111028), - *j.148* (NGB 111034) in Bonus, - *j.274* (NGB 111161), - *j.288* (NGB 111175), - *j.301* (NGB 111188), - *j.311* (NGB 111198), - *j.340* (NGB 111227), - *j.346* (NGB 111233), - *j.349* (NGB 111236), - *j.358* (NGB 111245), - *j.370* (NGB 111257), - *j.390* (NGB 111277), - *j.429* (NGB 111317), - *j.447* (NGB 111335), - *j.470* (NGB 111358) in Foma (CIho 11333) (7, 14); *cer-j.183* (NGB 111069), - *j.184* (NGB 111070), - *j.696* (NGB 111584) in Bonus, - *j.275* (NGB 111162), - *j.399* (NGB 111286), - *j.517* (NGB 111405), - *j.521* (NGB 111409), - *j.558* (NGB 111446) in Foma, - *j.1024* (NGB 111912), - *j.1081* (NGB 111969) in Carlsberg II (CIho 10114) (7); *cer-j.458* (NGB 111346) in Foma, - *j.780* (NGB 111668), - *j.797* (NGB 111685), - *j.832* (NGB 111720) in Bonus, - *j.1090* (NGB 111978), - *j.1102* (NGB 111990) in Kristina (NGB 1500) (8); *cer-j.909* (NGB 111797) in Bonus, - *j.1152* (NGB 112040) in Kristina (9); *cer-j.1204* (NGB 112092), - *j.1231* (NGB 112119), - *j.1233* (NGB 112121), - *j.1239* (NGB 112127), - *j.1251* (NGB 112139) in Kristina (10); *cer-j.997* (NGB 111885), - *j.1331* (NGB 112219), - *j.1361* (NGB 112249), - *j.1388* (NGB 112276), - *j.1405* (NGB 112293), - *j.1433* (NGB 112321), - *j.1469* (NGB 112357) in Bonus (10); *cer-j.1712* (NGB 112525), - *j.1744* (NGB 112558), - *j.1761* (NGB 112576), - *j.1803* (NGB 117351), - *j.1808* (NGB 117356) in Bonus (12); *cer-j.1827* (NGB 117375) in Bonus, - *j.1831* (NGB 117379), - *j.1835* (NGB 117383), - *j.1839* (NGB 117387), - *j.1841* (NGB 117389), - *j.1843* (NGB 117391), - *j.1844* (NGB 117392), - *j.1847* (NGB 117395), - *j.1850* (NGB 117398), - *j.1852* (NGB 117400), - *j.1857* (NGB 117405), - *j.1858* (NGB 117406), - *j.1860* (NGB 117408), - *j.1861* (NGB 117409), - *j.1862* (NGB 117410) in Sv 79353 (13).

Mutant used for description and seed stocks:

glf3.c (GSHO 577) in Goseshikoku; *cer-j.59* (NGB 110943, GSHO 431) in Bonus is used for allelic localization tests and for wax chemistry and wax structure studies; *glf3.d* from Gateway in Bowman (PI 483237)*5 (GSHO 2019); *glf3.d* in Bowman*8 (BW386, NGB

20624); *cer-j.59* in Bowman*3 (GSHO 2021); *cer-j.59* in Bowman*7 (BW114, NGB 20520).

References:

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2. Giese, B.N. 1976. Roles of the *cer-j* and *cer-p* loci in determining the epicuticular wax composition on barley seedling leaves. *Hereditas* 82:137-148.
3. Haus, T.E. 1974. Allelism tests of chromosome 4 mutants. *Barley Genet. Newsl.* 4:31-33.
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8. Lundqvist, U., and D. von Wettstein. 1973. Stock list for the eceriferum mutants II. *Barley Genet. Newsl.* 3:110-112.
9. Lundqvist, U., and D. von Wettstein. 1975. Stock list for the eceriferum mutants III. *Barley Genet. Newsl.* 5:88-91.
10. Lundqvist, U., and D. von Wettstein. 1977. Stock list for the eceriferum mutants IV. *Barley Genet. Newsl.* 7:92-96.
11. Lundqvist, U., and D. von Wettstein. 1982. Stock list for the eceriferum mutants VI. *Barley Genet. Newsl.* 12:169-172.
12. Lundqvist, U., and D. von Wettstein. 1985. Stock list for the eceriferum mutants VII. *Barley Genet. Newsl.* 15:89-93.
13. Lundqvist, U., and D. von Wettstein. 1988. Stock list for the eceriferum mutants VIII. *Barley Genet. Newsl.* 18:88-91.
14. Lundqvist, U., P. von Wettstein-Knowles, and D. von Wettstein. 1968. Induction of eceriferum mutants in barley by ionizing radiations and chemical mutagens. II. *Hereditas* 59:473-504.
15. Takahashi, R., J. Hayashi, and I. Moriya. 1962. Linkage studies. *Barley Newsl.* 5:41-42.
16. Takahashi, R., J. Hayashi, and I. Moriya. 1971. Linkage studies in barley. *Barley Genet. Newsl.* 1:51-58.
17. Takahashi, R., J. Hayashi, T. Konishi, and I. Moriya. 1972. Inheritance and linkage studies in barley V. Locating of seven new mutant genes. *Ber. Ohara Inst. landw. Biol., Okayama Univ.* 15:147-168.
18. Tsuchiya, T. 1973. Allelic relationship between two glossy seedling genes, *gl3* and *gl4* in barley. *Barley Genet. Newsl.* 3:66-67.
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21. Wettstein-Knowles, P. von, 1971. The molecular phenotypes of the *eceriferum* mutants. p. 146-193. *In* R.A. Nilan (ed). *Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969.* Washington State Univ. Press, Pullman.

Prepared:

R. Takahashi. 1972. Barley Genet. Newsl. 2:190.

T. Tsuchiya and T.E. Haus. 1971. Barley Genet. Newsl. 1:159 as BGS 256, Glossy leaf 4, *gl4*.

Revised:

T. Tsuchiya. 1980. Barley Genet. Newsl. 10:117 as BGS 165, Glossy seedling 3, *gl3*; and Barley Genet. Newsl. 10:123 as BGS 256, Glossy leaf 4, *gl4*.

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:190-191.

BGS 166, Male sterile genetic 25, *msg25*

Stock number: BGS 166
Locus name: Male sterile genetic 25
Locus symbol: *msg25*

Previous nomenclature and gene symbolization:

Male sterile = *msg*,*r* (7).

Inheritance:

Monofactorial recessive (2, 7).

Located in chromosome 4HL (1, 6); near the centromere and proximal from the *Blx1* (blue aleurone xenia 1) locus (6, 9).

Description:

Selfing - 0.7% for *msg25.r* (6), 2.6% for *msg25.dz* (3).

Outcrossing - complete female fertility (6).

Stamens - anthers smaller than fertile sib, but some have stomium. Some filament elongation may occur (6).

Origin of mutant:

A spontaneous mutant in Betzes (PI 129430) (6).

Mutational events:

msg25.r (MSS086, GSHO 744) in Betzes (PI 129430) (6); *msg25.dz* (MSS374) in Klages (CIho 15487) (3, 4, 5, 8).

Mutant used for description and seed stocks:

msg25.r (GSHO 744) in Betzes; *msg25.r* in Bowman (PI 483237)*7 (GSHO 2020, BW560, NGB 23428).

References:

1. Eslick, R.F. 1971. Balanced male steriles and dominant pre-flowering selective genes for use in hybrid barley. p. 292-297. In R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
2. Hockett, E.A. 1974. The genetic male sterile collection. Barley Genet. Newsl. 4:121-123.
3. Hockett, E.A. 1979. The genetic male sterile collection. Barley Genet. Newsl. 9:124-128.
4. Hockett, E.A. 1984. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl. 14:70-75.
5. Hockett, E.A. 1985. Coordinator's report. The genetic male sterile barley collection. Barley Genet. Newsl. 15:81.
6. Hockett, E.A., and R.F. Eslick. 1971. Genetic male-sterile genes useful in hybrid barley production. p. 298-307. In R.A. Nilan (ed.) Barley Genetics II. Proc. Second Int. Barley Genet. Symp., Pullman, WA, 1969. Washington State Univ. Press, Pullman.
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Prepared:

E.A. Hockett. 1974. Barley Genet. Newsl. 4:135 as BGS 386.

E.A. Hockett. 1975. Barley Genet. Newsl. 5:112.

Revised:

J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:192.

BGS 167, Reaction to barley yellow mosaic virus 1, *rym1*

Stock number: BGS 167
Locus name: Reaction to barley yellow mosaic virus 1 (BaYMV)
Locus symbol: *rym1*

Previous nomenclature and gene symbolization:

Resistance to BaYMV = *Ym* (8).

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosome 4HL (3, 5); approximately 9.7 cM distal from the *glf3* (glossy leaf 3) locus (3); closely linked to molecular marker MWG2134 (5), which is in 4H bin 06.

Description:

Plants with the *rym1.a* gene show less yellowing and stunting than susceptible plants when grown in fields that are infested with BaYMV (8). Mokusekko 3 is resistant to all strains of BaYMV and BaMMV (barley mild mosaic virus) in Japan (1, 6) and Germany (7), and possesses at least two recessive genes, *rym1.a* and *rym5.h* (3, 5). The *rym1.a* gene was separated from the *rym5.h* gene in the progeny from a cross between Mokusekko 3 and Colseess (a susceptible genetic stock) using isozyme assisted selection (3). The line MK501-234 carries only the *rym1.a* gene and is resistant to all strains of BaYMV in Japan (2, 3).

Origin of mutant:

Natural occurrence in Mokusekko 3 (OUC627, PI 420938) (8).

Mutational events:

rym1.a in Mokusekko 3 (PI 420938, OUC627) (8).

Mutant used for description and seed stocks:

rym1.a in Mokusekko 3 (OUC627, PI 420938) (3); *rym1.a* in MC501-234, which has only the *rym1.a* gene for resistance to BaYMV (3).

References:

1. Kashiwazaki, S., K. Ogawa, T. Usugi, T. Omura, and T. Tsuchizaki. 1989. Characterization of several strains of barley yellow mosaic virus. *Ann. Phytopath. Soc. Japan* 55:16-25.
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Prepared:

R.G. Timian. 1976. Barley Genet. Newsl. 6:125.

Revised:

J.D. Franckowiak and T. Konishi. 1996. Barley Genet. Newsl. 26:193.

T. Konishi and J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:96-97.

BGS 168, Globosum-a, *glo-a*

Stock number: BGS 168
Locus name: Globosum-a
Locus symbol: *glo-a*

Previous nomenclature and gene symbolization:
None.

Inheritance:
Monofactorial recessive (1).
Located in chromosome 4HS (1, 3).

Description:
Fertile spikelets are shortened and the resulting kernels are nearly round or globe-shaped. Sterile lateral spikelets are 1/2 normal length and twisted (3). In the Bowman backcross-derived line, the *glo-a.1003* allele reduces kernel size, test weight, and yield.

Origin of mutant:
An X-ray induced mutant in Proctor (PI 280420) (1, 3).

Mutational events:
glo-a.1003 (1343/63, GSHO 1328) in Proctor (PI 280420) (1, 2, 3).

Mutant used for description and seed stocks:
glo-a.1003 (GSHO 1328) in Proctor; *glo-a.1003* in Bowman (PI 483237)*7 (GSHO 2006, BW392, NGB 20630).

References:
1. Fischbeck, G., and H. Häuser. 1976. Research notes. Barley Genet. Newsl. 6:28-29.
2. Häuser, H., and G. Fischbeck. 1979. Genetic analysis of some induced mutants. Barley Genet. Newsl. 9:26-27.
3. Häuser, J., and G. Fischbeck. 1976. Untersuchungen zur Lokalisierung einiger Mutationen von Gerste (*Hordeum sativum*). Z. Pflanzenzücht. 77:269-280.

Prepared:
G. Fischbeck. 1978. Barley Genet. Newsl. 8:152.

Revised:
J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:194.

BGS 169, Light green 2, *lgn2*

Stock number: BGS 169
Locus name: Light green 2
Locus symbol: *lgn2*

Revised locus symbol:

Some confusion exists about the correct identity of the *lgn2.b* stock. The *lgn2.b* mutant may be at the same mutant as *lgn3.c* (see BGS 170), but this fact has not been confirmed by allelism tests because both are associated with same accession (GSHO 171).

Previous nomenclature and gene symbolization:

Light green 2 = *lg2* (1).
Light green 3 = *lg3* (2).

Inheritance:

Monofactorial recessive (2).
Located in chromosome 4HS (2); about 2.0 cM from the *Kap1* (hooded lemma 1) locus (2).

Description:

Seedlings have pale green color and are not viable (2). Greenhouse grown seedlings appear normal upon emergence, but later their color changes to pale green and they die (1). This mutant would need to be maintained as a heterozygous stock.

Origin of mutant:

A spontaneous mutant in an unknown cultivar (2), but labeled Minn. 75 and with a phenotype similar to Black Hulless.

Mutational events:

lgn2.b (GSHO 171) in an unknown cultivar (2).

Mutant used for description and seed stocks:

lgn2.b (GSHO 171) in an unknown cultivar.

References:

1. Haus, T.E. 1978. BGS 169, Light green-2, *lg2*. Barley Genet. Newsl. 8:153.
2. Immer, F.R., and M.T. Henderson. 1943. Linkage studies in barley. Genetics 28:419-440.

Prepared:

T.E. Haus. 1978. Barley Genet. Newsl. 8:153.

Revised:

J.D. Franckowiak. 2012. Barley Genet. Newsl. 42:264.

BGS 170, Light green 3, *lgn3*

Stock number: BGS 170
Locus name: Light green 3
Locus symbol: *lgn3*

Previous nomenclature and gene symbolization:

Light green 7 = *lg7* (3).

Light green 3 = *lg3*, the *lg3* stock studied by Hanson and Kramer (2) may not be the same as the *lg3* (GSHO 171) stock.

Inheritance:

Monofactorial recessive (1, 3).

Located in chromosome 4HL (1, 2, 4, 5); over 10.5 cM distal from the *Kap1* (hooded lemma 1) locus (2).

Description:

Seedlings have light or pale green color (3). The pale green color persists until near maturity, and plants are very weak (3) or non-viable in the field (2). Plants can be grown to maturity in greenhouses (4), but tillering is much reduced and seeds are very thin.

Origin of mutant:

A spontaneous mutant in an unknown cultivar (3, 4).

Mutational events:

lgn3.c (No 150, GSHO 171) in an unknown cultivar (3); *lgn3.g* (*lg7*) (No 154, GSHO 173) in an unknown cultivar (3).

Mutant used for description and seed stocks:

lgn3.c (GSHO 171) in an unknown cultivar; *lgn3.c* in Bowman (PI 483237)*5 (GSHO 2010); *lgn3.c* in Bowman*7 (BW480, NGB 20708).

References:

1. Hanson, W.D. 1952. An interpretation of the observed amount of recombination in interchange heterozygotes in barley. *Genetics* 37:90-100.
2. Hanson, W.D., and H.H. Kramer. 1949. The genetic analysis of two chromosome interchanges in barley from F₂ data. *Genetics* 34:687-700.
3. Immer, F.R., and M.T. Henderson. 1943. Linkage studies in barley. *Genetics* 28:419-440.
4. Tsuchiya, T., T. Fachan, and T.E. Haus. 1976. Primary trisomic analysis of *lg3* (light green) and *f3* (chlorina) in barley. *Barley Genet. Newsl.* 6:82-84.
5. Tsuchiya, T., and L.B. Hall. 1978. Telotrisomic analysis of four mutant genes in barley. *Barley Genet. Newsl.* 8:104-107.

Prepared:

T.E. Haus. 1978. *Barley Genet. Newsl.* 8:154.

Revised:

J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:195.

BGS 171, Light green 4, *lgn4*

Stock number: BGS 171
Locus name: Light green 4
Locus symbol: *lgn4*

Previous nomenclature and gene symbolization:

Light green 1 = *lg1* (2).
Light green 4 = *lg4* (2).
Light green 9 = *lg9* (2, 3).

Inheritance:

Monofactorial recessive (2, 5).
Located in chromosome 4HL (2, 4, 5, 6); about 5.0 cM distal from the *Kap1* (hooded lemma 1) locus (2, 4); about 4.0 cM proximal from the *glf1* (glossy leaf 1) locus (2, 4).

Description:

Seedlings are light green in color, and the light green color persists until near maturity (1). In the Bowman backcross-derived lines, mutant plants are weaker than normal sibs and produce thinner seeds.

Origin of mutant:

A spontaneous mutant in the progeny of the cross Himalaya X Ingrescens (2).

Mutational events:

lgn4.d (*lg1*) (GSHO 681) in Himalaya X Ingrescens (2); *lgn4.i* (*lg9*) (GSHO 1, GSHO 94) in No 156, an unknown cultivar (1, 2).

Mutant used for description and seed stocks:

lgn4.d (GSHO 681) in Himalaya X Ingrescens; *lgn4.d* in Bowman (PI 483237)*7 (GSHO 2011, BW481, NGB 20709).

References:

1. Haus, T.E. 1973. Allelism among light green, *lg*, seedling mutants. Barley Genet. Newsl. 3:17-18.
2. Immer, F.R., and M.T. Henderson. 1943. Linkage studies in barley. Genetics 28:419-440.
3. Robertson, D.W., G.A. Wiebe, and R.G. Shands. 1947. A summary of linkage studies in barley: Supplement I, 1940-1946. J. Am. Soc. Agron. 39:464-473.
4. Seip, L., and T. Tsuchiya. 1978. Trisomic analysis of *lg4* and *zb_c*. Barley Genet. Newsl. 8:86-89.
5. Singh, R.J., and T. Tsuchiya. 1974. Further information on telotrisomic analysis in barley. Barley Genet. Newsl. 4:66-69.
6. Tsuchiya, T., and R.L. Haines. 1975. Trisomic analysis of nine mutant genes in barley. Barley Genet. Newsl. 5:67-69.

Prepared:

T.E. Haus. 1978. Barley Genet. Newsl. 8:155.

Revised:

J. D. Franckowiak. 1997. Barley Genet. Newsl. 26:196.

BGS 172, Short awn 5, *lks5*

Stock number: BGS 172
Locus name: Short awn 5
Locus symbol: *lks5*

Previous nomenclature and gene symbolization:

Short awn 5 = *lk5* (7).
Breviaristatum-2 = *ari-2* (5, 6).
Breviaristatum-c = *ari-c.2* (6, 13, 14).

Inheritance:

Monofactorial recessive (6, 7).
Located in chromosome 4HL (15); about 6.9 cM distal from the *Kap1* (hooded lemma 1) locus (7, 9); near AFLP marker E4143-5 in subgroup 38 of the Proctor/Nudinka map (10); *lks5.f* is associated with SNP markers 1_0262 to 2_0072 (positions 76.26 to 95.92 cM) in 4H bin 06 of the Bowman backcrossed-derived line BW493 (2); *ari-c.2* is associated with SNP markers 2_0289 to 2_1322 (positions 69.62 to 112.64 cM) in 4H bins 05 to 08 of the Bowman backcrossed-derived line BW040 (2), in 4H bin 06; *lks5.p* isolated in genetic stocks BW474 and BW475 from the *le1* (lemma leafy 1) stock, G7118, *lks5.p* is associated with SNP markers 2_1122 to 1_1019 (positions 47.80 to 183.54) in 4H bins 05 to 13 of the Bowman backcrossed-derived line BW474 (2); *lks5.p* is associated with SNP markers 2_0422 to 2_0072 (positions 38.41 to 95.92 cM) in 4H bins 04 to 06 of the Bowman backcrossed-derived line BW475 (2).

Description:

Awns on both central and lateral spikelets are reduced to 1/4 or less of normal length in six-rowed cultivars (7). Only the central spikelets exhibit reduced awn length in two-rowed cultivars (3, 6). The rachilla is often modified, and in extreme cases the rachilla may develop as a malformed additional floret (7). Awns are thin and brittle (6). Plants of the Bowman backcross-derived line for *lks5.f*, BW493, had awns that extended 3 to 4 cm beyond the tip of the spike, while those of Bowman were 12 to 13 cm beyond the tip. Kernels of BW493 were slightly shorter, narrower (3.4 vs. 3.9 mm), and lighter (4.6 vs. 5.5 mg). BW493 plants were slightly taller than Bowman and grain yields were slightly reduced (4). Presence of the mutant allele *lks5.p* is needed for expression of the leafy lemma 1 (*le1.a*) gene (4, 10).

Origin of mutant:

A spontaneous mutant in an unknown cultivar (7).

Mutational events:

lks5.f (GSHO 1297) in Clho 5641 (7, 13); *lks5.g* (Kmut 218) in Asahi 5 (OUJ509) (13); *ari-c.2* (GSHO 1651, NGB 115847), -c.59 (NGB 115913) in Bonus (PI 189763), -c.103 (NGB 115915) in Foma (Clho 11333) (3); *ari-c.106* (NGB 115918) in Foma (5); *ari-c.109* (NGB 115921), -c.110 (NGB 115922), -c.111 (NGB 115923), -c.112 (NGB 115924), -c.120 (NGB 115932), -c.139 (NGB 115949), -c.157 (NGB 115967), -c.159 (NGB 115969), -c.179 (NGB 115989), -c.180 (NGB 115990), -c.199 (NGB 116008), -c.201 (NGB 116010), -c.203 (NGB 116012), -c.204 (NGB 116013), -c.206 (NGB 116014), -c.210a (NGB 116018), -c.210b (NGB 116019) -c.229 (NGB 116039) in Foma, -c.259 (NGB 116068), -c.262 (NGB 116071), -c.272 (NGB 116084), -c.276 (NGB 116089), -c.289 (NGB 116107), -c.291 (NGB 116111) in Kristina (NGB 1500) (6); *ari-c.307* (NGB 116135) in Kristina (8); two possible additional alleles have been reported, *lks5.h* (*lk.,f*) in two-rowed Glacier (3); and a mutant in Morex (Clho 15773) (12); *lks5.p* in G7118 (leafy lemma, GSHO 1780) mutant stock (1, 3, 4, 11).

Mutant used for description and seed stocks:

lks5.f (GSHO 1297) in Clho 5641; *ari-c.2* (NGB 115847, GSHO 1651) in Bonus; *lks5.f* in Bowman (PI 483237)*6 (GSHO 2014); *lks5.f* in Bowman*7 (BW493, NGB 20721); *ari-c.2* in Bowman*7 (GSHO 2013, BW040, NGB 20448); *lks5.p* from G7118 in Bowman*4 with *lel1.a* (BW474, NGB 20704); *lks5.p* from G7118 in Bowman*5 (BW475, NGB 20705).

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Prepared:

T.E. Haus. 1978. *Barley Genet. Newsl.* 8:156.

Revised:

- T. Tsuchiya. 1980. *Barley Genet. Newsl.* 10:119.
J.D. Franckowiak and U. Lundqvist. 1997. *Barley Genet. Newsl.* 26:197.
J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:110-111.

BGS 173, Non-blue aleurone xenia 3, *blx3*

Stock number: BGS 173
Locus name: Non-blue aleurone xenia 3
Locus symbol: *blx3*

Previous nomenclature and gene symbolization:

Non-blue aleurone 3 = *b/3* (1).

Complementary factors for blue vs white aleurone = *Bly* and *bly* (6).

Inheritance:

Monofactorial recessive when complementary dominant alleles are present at the *Blx1*, *Blx2*, *Blx4*, and *Blx5* loci (1, 2).

Located in chromosome 4HL (1, 2); close to the *blx1* (non-blue aleurone xenia 1) locus (1, 2, 6); over 25.3 cM distal from the *Kap1* (hooded lemma 1) locus (1, 5).

Description:

Blue aleurone color is due to anthocyanin pigments (4) which occur as lumps inside many aleurone granules in some or all aleurone cells (1). Variation in blue color expression from dark blue to an off-white is caused by environmental factors and modifying genes (1, 2). Aleurone color is best observed in well filled grain that is magnified to show individual aleurone cells, after more superficial tissues have been peeled off (3).

Origin of mutant:

Natural occurrence in a line selected from Composite Cross V (Clho 6620) (6).

Mutational events:

blx3.c in line Blx GSHO 2506) selected from Composite Cross V Clho 6620) (1).

Mutant used for description and seed stocks:

blx3.c in line Blx (GSHO 2506) selected from Composite Cross V.

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Prepared:

R.A. Finch. 1978. *Barley Genet. Newsl.* 8:165.

Revised:

J.D. Franckowiak and R.A. Finch. 1997. *Barley Genet. Newsl.* 26:198.

BGS 174, Non-blue (pink) aleurone xenia 4, *blx4*

Stock number: BGS 174
Locus name: Non-blue (pink) aleurone xenia 4
Locus symbol: *blx4*

Previous nomenclature and gene symbolization:

Non-blue (pink) aleurone 4 = *bl4* (3).

Inheritance:

Monofactorial recessive when complementary dominant alleles are present at the *Blx1*, *Blx2*, *Blx3*, and *Blx5* loci (3).

Located in chromosome 4HL (3); very close to the *blx1* (non-blue aleurone xenia 1) locus (3); over 29.5 cM distal from the *Kap1* (hooded lemma 1) locus (6).

Description:

Blue or pink aleurone color is due to pigments, known to be anthocyanin in the case of blue (5), which occur as lumps inside many aleurone granules in some or all aleurone cells (3). Variation in color expression from pink to an off-white is caused by environmental factors and modifying genes (3). The pink and red color aleurone colors are easier to observe in well filled grain that is magnified to show individual aleurone cells, after more superficial tissues have been peeled off (4). A brick red aleurone color results from the interaction of the *ibl* (intense blue aleurone) gene with the *blx4.d* gene in homozygotes (2, 3).

Origin of mutant:

Natural occurrence in a few Ethiopian and Nepalese lines (1, 2).

Mutational events:

blx4.d plus *ibl1.a* (intense blue aleurone 1) in Ethiopian 637 (GSHO 2508) (1); *blx4.d* only in Ab 6 (PI 548720, GSHO 2507), EP79, Grannenlose Zweizeilige (PI 548740) (3).

Mutant used for description and seed stocks:

blx4.d in Ab 6 (GSHO 2507).

References:

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6. Shim, J.W., and S.J. Suh. 1987. Linkage relationship of blue aleurone genes (*Bl*'s) in barley. p. 213-217. *In* S. Yasuda and T. Konishi (eds.) *Barley Genetics V. Proc. Fifth Int. Barley Genet. Symp.*, Okayama. 1986. Sanyo Press Co., Okayama.

Prepared:

R.A. Finch. 1978. *Barley Genet. Newsl.* 8:166.

Revised:

J.D. Franckowiak and R.A. Finch. 1997. *Barley Genet. Newsl.* 26:199.

BGS 176, Ovaryless 1, *ovl1*

Stock number: BGS 176
Locus name: Ovaryless 1
Locus symbol: *ovl1*

Previous nomenclature and gene symbolization:

Ovaryless = *ovl* (2, 3).

Inheritance:

Monofactorial recessive with very weak co-dominance (3).

Location in chromosome 4H (1, 5).

Description:

The homozygous recessive plant shows nonfunctional female reproductive parts, but anthers are well developed and pollen is viable. Spikes are nearly normal length but are awnless and completely sterile. Due to the lack of a midvein, the second and later leaves droop noticeably. Leaf length is slightly short than normal and leaf blades are somewhat narrower. The heterozygous plant has a midvein present in the basal half of the leaf, but it disappears toward the tip. As a result, some drooping is observed, but it is less apparent than in homozygous plants. Leaf length and width is nearly normal and the plant is fertile (2, 3). A viable source of this mutant has not been identified.

Origin of mutant:

A gamma ray induced mutant in Kanto Bansei Gold (Kanto Bansei Gall) (OUJ818) (2, 3).

Mutational events:

ovl1.a (Kmut 21b, GSHO 610) in Kanto Bansei Gold (OUJ818) (1).

Mutant used for description and seed stocks:

ovl1.a (GSHO 610) in Kanto Bansei Gold. The original stock carried both *ovl1.a* and a reciprocal translocation (T4-6) (3, 4).

References:

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Prepared:

T. Tsuchiya and L. Seip. 1980. BGS 168, Ovaryless (male), *ovl*. Barley Genet. Newsl. 10:118.

Revised:

T. Tsuchiya. 1983. Barley Genet. Newsl. 13:110. (The BGS number was changed to BGS 176.)

J.D. Franckowiak. 2005. Barley Genet. Newsl. 35:191.

BGS 178, Intermedium spike-c, *int-c*

Stock number: BGS 178
Locus name: Intermedium spike-c
Locus symbol: *int-c*

Previous nomenclature and gene symbolization:

Intensifer for $Z = W$ (22).
Infertile intermedium = *i* (12, 20, 21).
Allelic series I^h, I, i (12, 23).
Intermedium spike-c = *int-c* (6, 7, 17, 18).
Six-rowed spike 5 = *v5* (24).

Inheritance:

Monofactorial recessive (4, 5, 21, 24).
Located in chromosome 4HS (3, 5, 18, 21, 24); about 13.1 cM proximal from the *fch9* (chlorina seedling 9) locus (2, 3, 4, 5, 11); about 14.5 cM distal from the *Kap1* (hooded lemma 1) locus (2, 3, 4, 5, 11); about 3.5 cM from AFLP marker E4143-5 in subgroup 8 of the Proctor/Nudinka map (19).

Description:

Alleles at the *int-c* (*v5*) locus alter the size of lateral spikelets. The lemma apex of lateral kernels is rounded or weakly pointed, awnless or short-awned (1, 9, 16). Lower lateral spikelets may develop poorly in some *int-c* mutants (4), while seed development may occur in all lateral spikelets of others (6, 15). Variability in lateral spikelet development exists among the *int-c* mutants and environmental conditions can alter expressivity. The *Int-c.a* (formerly *I*) allele in six-rowed barley increases the size of lateral spikelets, while the *int-c.b* (formerly *i*) allele in two-rowed barley prevents anther development in lateral spikelets (9, 22). The *int-c.5* mutant in Bonus produces fertile stamens in lateral spikelets (9). In the presence of the *Int-c.h* (formerly I^h) allele of Mortoni, lateral spikelets are male fertile and may occasionally set seed (8, 12). Spikes of *vrs5.n* (*v5*) plants appear similar to those of six-rowed barley, but lateral spikelets are smaller (less than half the size of the central spikelets) and broader (3, 4).

Origin of mutant:

Natural occurrence in many two-rowed barley cultivars; an X-ray induced mutant in Gamma 4 (3, 5).

Mutational events:

int-c.b (*i*) in two-rowed barley (23); *Int-c.h* (I^h) in Mortoni (CIho 2210, GSHO 72) (8, 12); *vrs5.n* (*v5*) in Gamma 4 (38X-197, OUM338) (3, 5, 14); *int-c.5* (NGB 115423, GSHO 1765) in Bonus (PI 189763) (15, 18); *int-c.7* (NGB 115425), -c.62 (NGB 116835), -c.63 (NGB 115481) in Bonus, -c.13 (NGB 115431), -c.15 (NGB 115433), -c.16 (NGB 115434), -c.18 (NGB 115436), -c.25 (NGB 115443), -c.29 (NGB 115447) in Foma (CIho 11333), -c.33 (NGB 115451), -c.38 (NGB 115456), -c.45 (NGB 115463), -c.48 (NGB 115466), -c.49 (NGB 115467), -c.53 (NGB 115471), -c.56 (NGB 115474), -c.60 (NGB 115478) in Kristina (NGB 1500) (15); *int-c.70* (NGB 115488), -c.76 (NGB 115494), -c.78 (NGB 115496), -c.84 (NGB 115502) in Bonus, -c.95 (NGB 115513) in Hege (NGB 13692) (13).

Mutant used for description and seed stocks:

vrs5.n in Gamma 4 (GSHO 776); *int-c.b* in *Hordeum distichon* var. *nigrinudum* (GSHO 988); *int-c.5* (GSHO 1765) in Bonus; *int-c.b* from Compana (CIho 5438) in Bonneville (CIho 7248)*6 (CIho 16176) (10); *vrs5.n* from Gamma 4 in Bowman (PI 483237)*6 (GSHO 2002); *vrs5.n* in Bowman*7 (BW904, NGB 20788); *int-c.5* in Bowman*6 (GSHO 2003); *int-c.5* in Bowman*7 (BW421, NGB 20654).

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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. Barley Genet. Newsl. 26:200-201.

Revised:

U. Lundqvist and J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:237-239.

BGS 179, Hairy leaf sheath 1, *Hsh1*

Stock number: BGS 179
Locus name: Hairy leaf sheath 1
Locus symbol: *Hsh1*

Previous nomenclature and gene symbolization:

Hairy leaf sheath = *Hs* (7).

Inheritance:

Monofactorial dominant (4, 5, 6).

Located in chromosome 4HL (6); over 8.7 cM proximal from the *yhd1* (yellow head 1) locus (3, 5); over 22.5 cM distal from the *mlo* (reaction to *Erysiphe graminis hordei-o*) locus (3, 5); about 1.1 cM proximal from RFLP marker HVM067 in 4H bin 12 (2).

Description:

Short hairs (1 to 3 mm) are scattered or in rows on leaf sheaths of the basal part of the plant. The density of hairs varies considerably among cultivars and with changes in growing conditions. With few exceptions, no hairs are observed on the sheath of upper leaves (4, 5). Heterozygotes and smooth awned cultivars seem to have fewer hairs.

Origin of mutant:

Natural occurrence in a few cultivars and in some accessions of *Hordeum vulgare* subsp. *spontaneum* (1, 5, 6).

Mutational events:

Hsh1.a introduced into cultivated barley from its wild progenitor (5).

Mutant used for description and seed stocks:

Hsh1.a in Kimugi (GSHO 986, OUL012) (5, 6); *Hsh1.a* from R.I. Wolfe's Multiple Dominant Marker Stock (GSHO 3450) in Bowman (PI 483237)*10 (GSHO 2026, BW416, NGB 20649).

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Prepared:

R. Takahashi. 1972. Barley Genet. Newsl. 2:184 as BGS 158.

Revised:

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:202.

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:240-241.

BGS 180, Single internode dwarf 1, *sid1*

Stock number: BGS 180
Locus name: Single internode dwarf 1
Locus symbol: *sid1*

Previous nomenclature and gene symbolization:

Node-less dwarf = *nls* (4).

Inheritance:

Monofactorial recessive (2, 3).

Located in chromosome 4HL (4); over 13.2 cM distal from the *glf3* (glossy leaf 3) locus (2, 3); over 29.5 cM proximal from the *Kap1* (hooded lemma 1) locus (3, 4).

Description:

The mature plant has several culms, each having only a single elongated internode, the peduncle (4). Some of the elongated peduncles are much longer than normal. Plants are relatively weak and partially sterile, and have very lax spikes. The expression of mutant traits is less extreme in *sid1.b* plants, tillers often have two elongated internodes, fertility is better, and the spike is not as lax.

Origin of mutant:

An X-ray induced mutant in Akashinriki (OUJ659, PI 467400) from Dr Ohta (4).

Mutational events:

sid1.a (R101, OUX052, GSHO 2477) in Akashinriki (OUJ659, PI 467400) (2); *sid1.b* in (GSHO 2478) in Birgitta (NSGC 1870) (1).

Mutant used for description and seed stocks:

sid1.a (GSHO 2477) in Akashinriki; *sid1.a* in Bowman (PI 483237)*7 (GSHO 2024, BW849, NGB 22286); *sid1.b* in (GSHO 2478) in Birgitta; *sid1.b* in Bowman*8 (GSHO 2025, BW850, NGB 22287).

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Prepared:

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:203.

BGS 181, Early maturity 9, *eam9*

Stock number: BGS 181
Locus name: Early maturity 9
Locus symbol: *eam9*

Previous nomenclature and gene symbolization:

Early maturity c = *ea*,c (3, 4).

Inheritance:

Monofactorial recessive (3).

Located in chromosome 4HL (3); over 17.4 cM distal from the *Kap1* (hooded lemma 1) locus (4); over 15.6 cM proximal from the *glf3* (glossy leaf 3) locus (4).

Description:

Plants are about 4 weeks earlier under short-day conditions. At Kurashiki, Japan, maturity and agronomic effects of the *eam9.l* allele are similar to those of the photoperiod insensitive gene *eam8.k* (early maturity 8) (4, 5). The *eam9* is not allelic to several other early maturity genes that alter photoperiod sensitivity (1).

Origin of mutant:

Natural occurrence in Chinese cultivars from the lower basin of the Yangtze River (3).

Mutational events:

eam9.l in Tayeh 8 (OUC634, GSHO 1732) (3); Pao-an-chen 1 (OUC336), Pai-sha-pu 1 (OUC029), Mushin-chiang 3 (Mokusekko 3, OUC627, PI 420938), Yanghsin 2 (OUC327) (2, 3).

Mutant used for description and seed stocks:

eam9.l in Tayeh 8 (GSHO 1732). [*eam9.l* from DH6 in Bowman (PI 483237)*5 (GSHO 3422, BW291, NGB 20575), but the earliness gene in Bowman backcross lines is likely *Eam5.x*.]

References:

1. Gallagher, L.W. (Personal communications).
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Prepared:

J.D. Franckowiak and T. Konishi. 1997. Barley Genet. Newsl. 26:204.

BGS 182, Extra floret-a, *flo-a*

Stock number: BGS 182
Locus name: Extra floret-a
Locus symbol: *flo-a*

Previous nomenclature and gene symbolization:
None.

Inheritance:

Monofactorial recessive (3, 4).

Location in chromosome 6H (1); *flo-a.1* is associated with SNP markers 1_0539 to 1_0040 (positions 76.05 to 107.26 cM) in 6H bins 06 to 07 of the Bowman backcross-derived line BW367 (1); *flo-a.3* is associated with SNP markers 2_0746 to 1_1246 (positions 125.86 to 134.55 cM) in 6H bin 08 of the Bowman backcross-derived line BW368 (1); *flo-a.5* is associated with SNP markers 1_0061 to 1_1246 (positions 70.15 to 134.55 cM) in 6H bins 05 to 08 of the Bowman backcross-derived line BW369 (1), likely in 6H bin 07.

Description:

Extra bracts develop occasionally at the base of the central spikelet on the abaxial side. Formation of the extra bracts is most common in the central portion of the spike, but rarely will the bracts form another spikelet (2, 4). Except of the occasional development of a bract below the central spikelet, the Bowman backcross-derived lines for mutants at the *flo-a* locus, BW367, BW368, and BW369 were similar to Bowman (2).

Origin of mutant:

An ethylene imine induced mutant in Foma (CIho 11333) (4).

Mutational events:

flo-a.1 (NGB 114271, GSHO 1741) in Foma (CIho 11333) (4); *flo-a.3* (NGB 114273, GSHO 1742), previously named *flo-b.3* in Foma; *flo-a.5* (NGB 114275, GSHO 1743), previously named *flo-c.5* in Foma (4).

Mutant used for description and seed stocks:

flo-a.1 (GSHO 1741, NGB 114271) in Foma (*flo-a.3* (GSHO 1742, NGB 114273) in Foma; *flo-a.5* (GSHO 1743, NGB 114275) in Foma; *flo-a.1* in Bowman (PI 483237)*5 (GSHO 2005), in Bowman*7 (BW367, NGB 20606); *flo-a.3* in Bowman (PI 483237)*6 (GSHO 2128, BW368, NGB 20607); *flo-a.5* in Bowman (PI 483237)*7 (GSHO 1877, BW369, NGB 20608).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2011. Genetic dissection of barley morphology and development. *Plant Physiol.* 155:617-627.
2. Franckowiak, J.D. (Unpublished).
3. Gustafsson, Å., A. Hagberg, U. Lundqvist, and G. Persson. 1969. A proposed system of symbols for the collection of barley mutants at Svalöv. *Hereditas* 62:409-414.
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Prepared:

U. Lundqvist and J.D. Franckowiak. 1997. *Barley Genet. Newsl.* 26:205.

Revised:

J.D. Franckowiak and U. Lundqvist. 2011. *Barley Genet. Newsl.* 41:112.

BGS 183, Yellow node 1, *Ynd1*

Stock number: BGS 183
Locus name: Yellow node 1
Locus symbol: *Ynd1*

Previous nomenclature and gene symbolization:

Yellow node = *Yn* (R.F. Eslick's collection notes) (1).

Inheritance:

Monofactorial incomplete dominant (1).

Located in chromosome 4HS (2); based on incomplete data from the Harrington/Morex mapping population (2); linkage drag with the *int-c* (intermedium spike -c) locus (1).

Description:

Nodes of the culm appear to lack a coating of surface waxes in plants homozygous for the *Ynd1.a* gene. In heterozygotes, surface waxes may be observed on the upper half of the node. This trait is easier to observe in greenhouse grown plants where surface waxes are not rubbed off by wind caused leaf movements. The *Ynd1.a* allele is present in many six-rowed cultivars of Oriental origin (1). The glossy node trait is seldom found in two-rowed lines selected from two- by six-rowed crosses because the *Ynd1.a* allele is closely linked to the *Int-c.a* allele, which increases the size of lateral spikelets (1, 2).

Origin of mutant:

Naturally occurring in many six-rowed barley cultivars (1).

Mutational events:

Ynd1.a in a stock from R.F. Eslick's collection at Montana State University, Bozeman (GSHO 1607) (1).

Mutant used for description and seed stocks:

Ynd1.a in Morex (CIho 15773, GSHO 2492); *Ynd1.a* from Sen 'S' (GSHO 1605) in Bowman (PI 483237)*6 (GSHO 2363); *Ynd1.a* in Bowman*7 (BW923, NGB 22352).

References:

1. Franckowiak, J.D. (Unpublished).
2. Kleinhofs, A., and J.D. Franckowiak. (Unpublished).

Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:98.

BGS 184, Zeocriton 3, Zeo3

Stock number: BGS 184
Locus name: Zeocriton 3
Locus symbol: Zeo3

Previous nomenclature and gene symbolization:

Semidwarf mutant = Mo1 (5).
Zeocriton h = *Zeo.h* (2).

Inheritance:

Monofactorial dominant (2).
Location in chromosome 4HS (2); based on linkage drag with the *int-c* (intermedium spike-c) locus (2).

Description:

Spikes have compact appearance and are about 3/4 normal length because rachis internodes are shorter than those of normal sibs, 3.3 vs. 4.1 mm. The spike remains strap-shaped because all rachis internodes are about the same length. Plants are about 10 cm shorter than normal sibs (1).

Origin of mutant:

A sodium azide induced mutant in Morex (Clho 15773) (5).

Mutational events:

Zeo3.h (Wa11094-81, DWS1259) in Morex (3); renamed *Zeo2.h* based on SNP molecular marker studies indicating allelism for BW940 at the *Zeo2* locus in 2HL (1).

Mutant used for description and seed stocks:

Zeo2.h (GSHO 1611) in Morex; *Zeo2.h* in Bowman (PI 483237)*7 (GSHO 1999, BW940, NGB 22369).

References:

1. Franckowiak, J.D. (Unpublished).
2. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. *Barley Genet. Newsl.* 24:63-70.
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Prepared:

J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:99.

BGS 185, Brachytic 5, *brh5*

Stock number: BGS 185
Locus name: Brachytic 5
Locus symbol: *brh5*

Previous nomenclature and gene symbolization:

Brachytic-m = *brh.m* (3).

Inheritance:

Monofactorial recessive (3, 5).

Located in chromosome 4HS (4); near the *int-c* (intermedium spike-c) locus (4); about 13.0 cM proximal from SSR marker Bmac0310 near the boundary between 4H bins 06 and 07 (1).

Description:

Plants are about 3/4 normal height and awns are about 3/4 of normal length. Peduncles are less than 2/3 normal length. Seedling leaves of *brh5* plants are relatively short. The kernels of *brh5* plants are shorter than those of normal sibs and weigh about 30% less. Plants lodge easily and the grain yield is about 1/2 normal (1, 2).

Origin of mutant:

A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (6).

Mutational events:

brh5.m (17:18:2, DWS1010, GSHO 1678 in Birgitta (NSGC 1870, NGB 14667) (5, 6).

Mutant used for description and seed stocks:

brh5.m (GSHO 1678 in Birgitta); *brh5.m* in Bowman (PI 483237)*7 (GSHO 2001, BW096, NGB 20502).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. *J. Hered.* 96:654-662.
2. Franckowiak, J.D. (Unpublished).
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5. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
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Prepared:

J.D. Franckowiak. 2002. *Barley Genet. Newsl.* 32:100.

Revised:

J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:242.

BGS 186, Slender dwarf 3, *sld3*

Stock number: BGS 186
Locus name: Slender dwarf 3
Locus symbol: *sld3*

Previous nomenclature and gene symbolization:

Anthocyanin-free = *ant-567* (6).
Proanthocyanidin-free 17.567 = *ant17.567* (5).
Slender dwarf e = *sld.e* (4).

Inheritance:

Monofactorial recessive (2).
Located in chromosome 4HS (3); based on linkage drag with the *int-c* (intermedium spike-c) locus (3); associated SNP markers 1_0208 to 2_0777 (positions 5.24 to 40.15 cM) in 4H bins 01 to 04 of the Bowman backcross-derived line BW863 (1).

Description:

The mutant gene *sld3.e* was isolated as a second mutant in the stock *ant17.567* (proanthocyanidin-free 17) (2). Plants show reduced vigor and are about 3/4 normal height. The number of spikelets per spike is about 3/4 that of normal sibs and kernels are slightly smaller. Rachis internodes can be slightly longer and grain yields are about 3/4 of normal. The Bowman backcross-derived line BW863 for *sld3.e* did not show a reduction in anthocyanin pigmentation or a large reduction in kernel size (2). Plants of BW863 were about 10% shorter than Bowman and peduncles were about 20% shorter. Rachis nodes were slightly longer and kernels per spike can be reduced up to 20% in some environments. Kernels were slightly shorter and thinner than those of Bowman and seed weights were 10 to 15% less. Grain yields were slightly reduced compared to those of Bowman (2).

Origin of mutant:

A sodium azide induced mutant isolated with *ant.567* in Manker (CIho 15549) (6).

Mutational events:

sld3.e (*ant17.567*, DWS1050) in Manker (CIho 15549) (2).

Mutant used for description and seed stocks:

sld3.e (GSHO 2480) in Bowman/*ant17.567*; *sld3.e* in Bowman (PI 483237)*7 (GSHO 1998, BW863, NGB 22300).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. Plant Physiology. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. Notes on linkage drag in Bowman backcross derived lines of spring barley. Barley Genet. Newsl. 24:63-70.
4. Franckowiak, J.D. 1999. Coordinator's report: Semidwarf genes. Barley Genet. Newsl. 29:74-79.
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Prepared:

J.D. Franckowiak. 2002. Barley Genet. Newsl. 32:101.

Revised:

J.D. Franckowiak. 2007. Barley Genet. Newsl. 37:243.

BGS 187, Brachytic 9, *brh9*

Stock number: BGS 187
Locus name: Brachytic 9
Locus symbol: *brh9*

Previous nomenclature and gene symbolization:

Brachytic-k = *brh.k* (3).

Inheritance:

Monofactorial recessive (3, 4).

Located in chromosome 4HS (1); about 11.7 cM distal from SRR marker Bmac0310 in 4H bin 06 (1).

Description:

Culms and peduncles are about 3/4 normal length and awns are 3/4 to 5/6 of normal length. Rachis internodes are slightly shorter than those of normal sibs. Seedling leaves of *brh9* plants are relatively short. The kernels of *brh9* plants are shorter and kernel weight are about 20% lower than those of normal sibs. Grain yields averaged less than 1/2 normal (1, 2); however, plants appeared nearly normal when grown in Dundee, Scotland (2). The *brh9.k* gene was found to non-allelic at *brh5* locus, which is located in the same region of 4HS (1).

Origin of mutant:

A sodium azide induced mutant in Birgitta (NSGC 1870, NGB 1494, NGB 14667) (5).

Mutational events:

brh9.k (17:14:4, DWS1006, GSHO 1676) in Birgitta (NSGC 1870, NGB 14667) (4, 5).

Mutant used for description and seed stocks:

brh9.k (GSHO 1676) in Birgitta; *brh9.k* in Bowman (PI 483237)*6 (GSHO 2170); *brh9.k* in Bowman*7 (BW101, NGB 20507).

References:

1. Dahleen, L.S., L.J. Vander Wal, and J.D. Franckowiak. 2005. Characterization and molecular mapping of genes determining semidwarfism in barley. *J. Hered.* 96:654-662.
2. Franckowiak, J.D. (Unpublished).
3. Franckowiak, J.D. 1995. The brachytic class of semidwarf mutants in barley. *Barley Genet. Newsl.* 24:56-59.
4. Franckowiak, J.D., and A. Pecio. 1992. Coordinator's report: Semidwarf genes. A listing of genetic stocks. *Barley Genet. Newsl.* 21:116-127.
5. Lehmann, L.C. 1985. (Personal communications).

Prepared:

J.D. Franckowiak and L.S. Dahleen. 2007. *Barley Genet. Newsl.* 37:244.

BGS 189, Accordion rachis 2, *Acr2*

Stock number: BGS 189
Locus name: Accordion rachis 2
Locus symbol: *Acr2*

Previous nomenclature and gene symbolization:

Lax spike = *lax* (4, 9, 11).
Accordion rachis = *acr* (7, 9, 12).
Accordion rachis 1 = *acr1.a* (6).
Accordion rachis b and c = *acr.b*, *acr.c* (3, 5).
Laxatum spike stocks = *Lax.aa*, *Lax.ab*, *Lax.am*, *lax.ao*, (5, 12).

Inheritance:

Monofactorial incomplete dominant for lax spike, one of three factors required for expression of accordion rachis trait (5, 12).
Located in chromosome 4HL (3); associated with SNP markers 1_0123 to 2_1018 (positions 158.82 to 183.54 cM) in 4HL of the Bowman backcross-derived lines BW445; Bowman backcross-derived lines BW007, BW008, BW009, BW439, BW444, and BW456 have identical heterogeneous SNP markers in 4HL, but their segments from the donor parent are longer (3), in 4H bins 11 or 12.

Description:

Rachis internodes are elongated and kernels appear longer than normal. The *Acr2* gene is in the second of three chromosomal regions associated with expression of the accordion rachis trait in Bowman backcross-derived lines BW009 and BW439. The long rachis internode trait was specifically added to the original accordion rachis stock by R.I. Wolfe (12). Characteristics associated with variants at the *Acr2* locus are difficult to determine because only the Bowman backcross-derived line BW444 (*Lax.aa* or *Acr2.aa*) did not have more than one chromosome segment from its donor parent (3). The rachis internodes of BW444 plants were about 30% longer, 5.7 vs. 4.4 mm, than those of Bowman. Leaf blades were slightly longer and wider. Kernels were slightly longer and heavier, 61 vs. 58 mg. Grain yields were equal or slightly more than those of Bowman. The donor parent (FN280) of the BW444 line traces to the lines developed by M.L. Martini and H.V. Harlan (8) in Idaho via crosses to six-rowed barley made by D.C. Rasmusson (10). The Bowman backcross-derived lines BW007 (*Acr2.b2*) and BW008 (*Acr2.c2*) had the identical segment of chromosome 4HL plus a 1H segment retained from their donor parents; however, the 1H segments in these lines differed for SNP marker patterns (3). The Bowman lines BW007 and BW008 are 10 to 15% taller than Bowman. The rachis internodes of BW007 are about 25% longer than those of Bowman, 4.7 vs. 3.7 mm., Burma Girl (GSHO 1071, *Acr2.b2*), the original stock for BW007, has several sterile rachis nodes at the base of the spike before spikelet development is initiated (4). BW007 had kernel weights that varied across experiments from smaller to slightly larger than those of Bowman. The rachis internodes of BW008 were nearly twice as long as those of Bowman, 8.2 vs. 4.5 mm, but they did not show the accordion-like bending associated with the accordion phenotype. Kernels of the BW008 line were slightly longer and heavier than those of Bowman (5). Two other Bowman backcross-derived lines, BW439 and BW456, have the 4HL SNP pattern associated with the *Acr2* locus. Both originate from the same donor stock AB1398 (GSHO 1115) from Aberdeen, Idaho and are assigned the gene symbol *Acr2.am*. BW456 was selected based on lax spikes while BW439 was selected based on tall plants (5).

Origin of mutant:

A naturally occurring deviant possibly in Long Rachis Internode (CIho 6164), developed by M.L. Martini and H.V. Harlan (8), or Burma Girl (CIho 14831), donated to the USDA Small Grains Collection by G.A. Wiebe. The *Acr2* gene has been incorporated into several genetic stocks from that source.

Mutational events:

Acr2.b2 in Burma Girl (CIho 14831, GSHO 1071) (5, 12); *Acr2.aa* in FN280 (GSHO 1572) (5, 10); *Acr2.ab* in ACBV89B229 (GSHO 1617) and ACBV89B232 (GSHO 1573) (12); *Acr2.c2* in T188 (GSHO 1480) from R.W. Woodward (2); *Acr2.am* in AB 1398 [GSHO 1115, likely CIho 14785 from G.A. Wiebe (1)]; all alleles may have been derived from one stock (3, 5).

Mutant used for description and seed stocks:

Acr2.aa in FN280 (GSHO 1572); *Acr2.b2* in Burma Girl (GSHO 1071); *Acr2.a2* in ACBV89B229 (GSHO 1617); *Acr2.c2* in T188 (GSHO 1480); *Acr2.am* in AB 1398 (GSHO 1115); *Acr2.a2* from ACBV89229 in Bowman*4 (GSHO 1899); *Acr2.a2* in Bowman*7 (BW009, NGB 20417 and BW439, NGB 20671); *Acr2.aa* from FN280 in Bowman*4 (GSHO 2276); *Acr2.aa* in Bowman*5 (BW444, NGB 20676); *Acr2.ab* from ACBV89B232 (GSHO 1573) in Bowman*4 (GSHO 2277); *Acr2.ab* in Bowman*6 (BW445, NGB 20677); *Acr2.b2* from Burma Girl in Bowman *2 (GSHO 1898); *Acr2.b2* in Bowman*5 (BW007, NGB 20415); *Acr2.c2* from T188 in Bowman*6 (BW008, NGB 20416); *Acr2.am* from AB 1398 in Bowman*4 (BW456, NGB 20688).

References:

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7. Haus, T.E. 1957. Inheritance of rachis internode length and an abnormal rachis type in barley. Dissertation Abstr. 49:179-180.
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Prepared:

J.D. Franckowiak 2010. Barley Genet. Newsl. 40:65-66.

BGS 190, Thick filament 1, *tfm1*

Stock number: BGS 190
Locus name: Thick filament 1 (male sterile genetic)
Locus symbol: *tfm1*

Previous nomenclature and gene symbolization:

None.

Inheritance:

Monofactorial recessive (2).

Located in chromosome 1HL (1); associated with SNP markers 2_0603 to 2_0915 (positions 199.04 to 202.94 cM) in 1HL of a heterozygous plant from the Bowman backcrossed-derived line BW877 (1), in 1H bin 14.

Description:

The filaments supporting the anthers are much thicker than normal, having a stalk-like appearance and a light green color. Since the filaments do not elongate, the mutant plants are largely male-sterile. Pollen fertility is apparently normal because mutant segregates will set a few seeds. Besides very poor seed, *tfm1* plants in Bowman backcross-derived line BW877 appear normal (2).

Origin of mutant:

A spontaneous mutant in the Volla (PI 280423) induced mutant 7060 backcrossed twice to Bowman (PI 483237) (2).

Mutational events:

tfm1.a from Volla 7060/2*Bowman (2).

Mutant used for description and seed stocks:

tfm1.a from Volla 7060/2*Bowman; *tfm1.a* in Bowman*7 (BW877, NGB 22311).

References:

1. Druka, A., J. Franckowiak, U. Lundqvist, N. Bonar, J. Alexander, K. Houston, S. Radovic, F. Shahinnia, V. Vendramin, M. Morgante, N. Stein, and R. Waugh. 2010. Genetic dissection of barley morphology and development. Plant Physiology. Epubl. 2010 November 18, 2010 as DOI:10.1104/pp110.166249.
2. Franckowiak, J.D. (Unpublished).

Prepared:

J.D. Franckowiak. 2010. Barley Genet. Newsl. 40:67.

BGS 191, Chlorina seedling 17, *fch17*

Stock number: BGS 191
Locus name: Chlorina seedling 17
Locus symbol: *fch17*

Previous nomenclature and gene symbolization:

Very yellow 3 = *vy3* (3).
Chlorina seedling *vy* = *fch.vy* (3).

Inheritance:

Monofactorial recessive (2).
Located in chromosomes 1HL or 3HL (1); associated with SNP markers 1_0830 to 2_0940 (positions 130.68 to about 179 cM) in 1HL and SNP markers 2_0130 to 1_0343 (positions 151.97 to 255.13 cM) in 3HL of the Bowman backcrossed-derived line BW344 (1).

Description:

Seedlings are pale yellow with a slight mottled type streaking and vigor is poor. The second leaf blade is chlorina with the tip gradually turning. Mature plants are normal green and have apparently normal vigor (3). In the Bowman backcross-derived line BW344, heading date was delayed by about 9 days compared to Bowman and grain yields were 50 to 70% of normal. Other morphological traits of BW344 plants were similar to those of Bowman (2). A new gene symbol is assigned to the *vy3* mutant because no other chlorina mutant with a similar phenotype, except *fch7*, is associated with either 1HL or 3HL (1, 2).

Origin of mutant:

A spontaneous mutant in Himalaya X Ingrescens (GSHO 681) (3).

Mutational events:

fch17.vy (E 37-517, NSL 30243, GSHO 1079) in Himalaya X Ingrescens (GSHO 681) (2, 3).

Mutant used for description and seed stocks:

fch17.vy (GSHO 1079) from Himalaya X Ingrescens; *fch17.vy* in Bowman (PI 483237)*5 (BW344, NGB 22139).

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